FIGURE 1

R35464	GCCC	GGGTC	: ITTCT	CGCCT	GGCTG	GGATC	GCTGCTCC	TC TCT	GGGGTCC	50
ORF							C S			16
				GAACG	CAGCA	TCCAC	GACTTCTG	CC TGG	TGTCGAA	100
ORF	M 5	A C	R	E R	S I	Н	D F C	L V	' S K	33
							TAGGTGGT			
ORF	V (/ G	R £	R A	S	M P	R W W	Υ.,	N V I	50
							GGGGCTGT			200
ORF	D	G S	C Q	L	F V	Y G	G C	D G	N 5	55
	AATAA	TTACC	TGACCA	LAGGA	GGAGT	GCCTC	AAGAAATG	TG CCA	CTGTCAC	250
ORF	N N	Y L	T	Ξ	Ε C	L	K K C	A I	· v ·	8 3
				GACC	TGGCC	ACCAG	CAGGAATG	CA, GCG	GATTCCT	300
ORF	E N	A	T G	D L	A	T S	RNA	X	D S S	100
							CTTGAAGA	CC ACT	TCAGCGA	350
ORF	V	P S	A P	R	R 2	D S	• .R	P L	Q R	116
	TATGT	TTCAA	NTATTO	NAAG	AATAA	TTGCA	CCGNCAAC	GN ATT		393
ORF	YV	s •	I •	R	I I	λ	P • I	•		130

KEY

R35464 - Nucleic acid sequence of EST R35464 (SEQ ID NO: 12)
ORF - EST R35464 Open Reading Frame Translation (SEQ ID NO: 13)

FIGURE 2

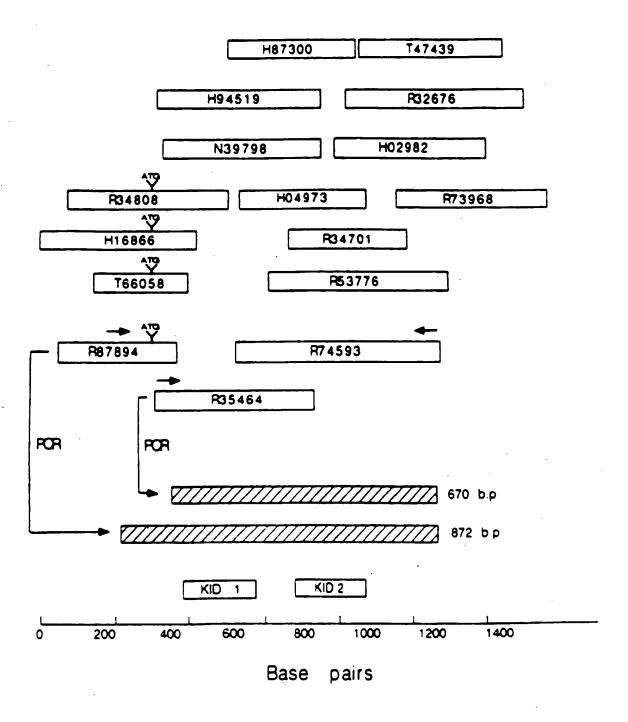
874593	GCAATAATTA	CCTGACCAAG	GAGGAGTGCC	TCAAGAAATG	TGCCACTGTC	50
ORF	g · L	5 D 3 C	G V P	QEM	CHCH	17
974593	ACAGAGAATG	CCACGGGTGA	CCTGGCCACC	AGCAGGAATG	CAGCGGATTC	100
ORF	R E C	H G *	P G H Q	Q E C	S G F	33
R74593	CTCTGTCCCA	AGTCTCCCAG	AAGGCAGGAT	TCTGAAGACC	ACTCCAGCGA	150
C F	L C P K	S P R	R Q D	S E D H	\$ S D	ن ي
R74593	TATGTTCAAC	TATGAAGAAT	ACTGCACCGC	CAACGCAGTC	ACTGGGCCTT	200
ORF	M F N	Y E E Y	C T A	N A V	T G P C	67
R74593	GCCGTGCATC	CTTCCCACGC	TGGTACTTTG	ACGTGGAGAG	GAACTCCTGC	250
ORF	R A S	FPR	WYFD	VER	N.S.C	83
R74593	AATAACTTCA	TCTATGGAGG	CTGCCGGGGC	AATAAGAACA	GCTACCGCTC	300
ORF	N N F I	Y G G	C R G	и к и ѕ	YRS	100
R74593	TGAGGAGGCC	TGCATGCTCC	GCTGCTTCCG	CCAGCAGGAG	ANTCCTCCCC	350
ORF	A 3 2	CMLR	CFR	Q Q E	NPPL	117
R74593	TGCCCCTTGG	CTCAMAGGTG	GTGGTTCTGG	CCGGGGCTGT	TTCGTGATGG	400
ORF	P L G	s k v	VVLA	G A V	S • W	133
R74593	TGTTGATCCT	TTTCCTGGGG	AGCNTCCATG	GTCTTACTG	TTCCGGGTGG	450
ORF	-		A S M			150
R74593	CAAGGAGGAA	CCAGGAGCGT	GCCCTGCGGA	NCGTCTGGAG	CTTCGGAGAT	500
ORF	K E E	P G A C	PAX	R L E	LRR.	101
R74593	GACAAGGGNT	•				510
ORF	0 G					169

R74593 - Nucleic acid sequence of EST R74593 (SEQ ID NO: 14)
ORF - EST R74593 Open Reading Frame Translation (SEQ ID NO: 15)

R35464	GGCCGGGTCGT TTCTCGCCTG GCTGGGA-TC GCTGCTCCTC TCTGGGGTC	CC 50
N39798	TGGGANTC GCTGCTCCTC TCTGGGGTC	CC 29
H94519	GCHGCG-CGT THNTCGCHT- GCTGGGA-TC GCTGCACCTC TCTGGGGTC	CG 47
R74593 corr.		
Consensus	GGCCGGGTCGT TTCTCGCCTG GCTGGGA-TC GCTGCTCCTC TCTGGGGT	CC 30
Translation	AGSF LAW LG S L L L S G V	- 3
R35464	TGGCCGGCCG ACCGAGAACG CAGCATCCAC GACTTCTGCC TGGTGTCG.	AA 100
N39798	TGG-CGGCCG ACCGAGAACG CAGCATCCAC GACTTCTGCC TGGTGTCG	AA 77
H94519	NGG-CGGCCG ACCGAGAACG CAGCATCCAC GACTTCTGCC TGGTGTCG	AA 96
R74593 corr.		
Consensus	TGG-CGGCCG ACCGAGAACG CAGCATCCAC GACTTCTGCC TGGTGTCG	5AA 99
Translation		<u>K</u> 15
R35464	GGTGGTGGGC AGATTCCGGG CCTCCATGCC TAGGTGGTGG TACAATGT	CA 150
N39798	GGTGGTGGGC AGATGCCGGG CCTCCATGCC TAGGTGGTGG TACAATGT	CA 127
H94519	GGTGGTGGGC AGATGCCGGG CCTCCATGCC TAGGTGGTGG TACAATGT	CA 146
R74593 corr.		
Consensus	GGTGGTGGGC AGATGCCGGG CCTCCATGCC TAGGTGGTGG TACAATG	TCA 149
Translation	Y Y G B C B A S M P B M M Y N Y	= 32
R35464	CTGACGGATC CTGCCAGCTG TTTGTGTATG GGGGCTGTGA CGGAAAC	AGC 200
N39798	CTGACGGATC CTGCCAGCTG TTTGTGTATG GGGGCTGTGA CGGAAAC	AGC 177
H94519	CTGACGGATC CTGCCAGCTG TTTGTGTATG GGGGCTGTGA CGGAAAC	AGC 196
R74593 corr.		-GC 2
Consensus	CTGACGGATC CTGCCAGCTG TTTGTGTATG GGGGCTGTGA CGGAAAC	AGC 199
Translation		<u>s</u> 48
	•	
R35464	AATAATTACC TGACCAAGGA GGAGTGCCTC AAGAAATGTG CCACTGT	CAC 250
N39798	AND AND THE TOTAL CONCERNED AND AND AND THE CONCERNED	
	ANTANTIACC TGACCAAGGA GGAGIGCCIC AAGAANIGIG COACIGI	CAC 221
H94519	ANTANTIACO TGACCAAGGA GGAGTGCCTC AAGAAATGTG CCACTGT AATAATTACO TGACCAAGGA GGAGTGCCTC AAGAAATGTG CCACTGT	CAC 246
H94519 R74593 corr.	AATAATTACC TGACCAAGGA GGAGTGCCTC AAGAAATGTG CCACTGT AATAATTACC TGACCAAGGA GGAGTGCCTC AAGAAATGTG CCACTGT	CAC 246
R74593 corr.	AATAATTACC TGACCAAGGA GGAGTGCCTC AAGAAATGTG CCACTGT AATAATTACC TGACCAAGGA GGAGTGCCTC AAGAAATGTG CCACTGT AATAATTACC TGACCAAGGA GGAGTGCCTC AAGAAATGTG CCACTGT	CAC 246 CAC 52 CAC 249
	AATAATTACC TGACCAAGGA GGAGTGCCTC AAGAAATGTG CCACTGT AATAATTACC TGACCAAGGA GGAGTGCCTC AAGAAATGTG CCACTGT AATAATTACC TGACCAAGGA GGAGTGCCTC AAGAAATGTG CCACTGT	CAC 246 CAC 52 CAC 249
R74593 corr. Consensus	AATAATTACC TGACCAAGGA GGAGTGCCTC AAGAAATGTG CCACTGT AATAATTACC TGACCAAGGA GGAGTGCCTC AAGAAATGTG CCACTGT AATAATTACC TGACCAAGGA GGAGTGCCTC AAGAAATGTG CCACTGT N N Y L T K E E C L K K C A T V	CAC 246 CCAC 52 CCAC 249 T 65
R74593 corr. Consensus Translation	AATAATTACC TGACCAAGGA GGAGTGCCTC AAGAAATGTG CCACTGT AATAATTACC TGACCAAGGA GGAGTGCCTC AAGAAATGTG CCACTGT AATAATTACC TGACCAAGGA GGAGTGCCTC AAGAAATGTG CCACTGT N N Y L T K E E C L K K C A T V AGAGAATGCC ACGGGTGACC TGGCCACCAG CAGGAATGCA GCGGATT	TCAC 246 TCAC 52 TCAC 249 T 65
R74593 corr. Consensus Translation R35464	AATAATTACC TGACCAAGGA GGAGTGCCTC AAGAAATGTG CCACTGT AATAATTACC TGACCAAGGA GGAGTGCCTC AAGAAATGTG CCACTGT AATAATTACC TGACCAAGGA GGAGTGCCTC AAGAAATGTG CCACTGT N N Y L T K E E C L K K C A T V AGAGAATGCC ACGGGTGACC TGGCCACCAG CAGGAATGCA GCGGATT AGAGAATGCC ACGGGTGACC TGGCCACCAG CAGGAATGCA GCGGATT	TCAC 246 TCAC 52 TCAC 249 T 65 TCCT 300 TCCT 277
R74593 corr. Consensus Translation R35464 N39798	AATAATTACC TGACCAAGGA GGAGTGCCTC AAGAAATGTG CCACTGT AATAATTACC TGACCAAGGA GGAGTGCCTC AAGAAATGTG CCACTGT AATAATTACC TGACCAAGGA GGAGTGCCTC AAGAAATGTG CCACTGT N N Y L T K E E C L K K C A T V AGAGAATGCC ACGGGTGACC TGGCCACCAG CAGGAATGCA GCGGATT AGAGAATGCC ACGGGTGACC TGGCCACCAG CAGGAATGCA GCGGATT AGAGAATGCC ACGGGTGACC TGGCCACCAG CAGGAATGCA GCGGATT	TCAC 246 TCAC 52 TCAC 249 T 65 TCCT 300 TCCT 277 TCCT 296
R74593 corr. Consensus Translation R35464 N39798 H94519	ANTANTIACO TGACCAAGGA GGAGTGCCTC AAGAAATGTG CCACTGT AATAATTACO TGACCAAGGA GGAGTGCCTC AAGAAATGTG CCACTGT AATAATTACO TGACCAAGGA GGAGTGCCTC AAGAAATGTG CCACTGT N N Y L T K E E C L K K C A T V AGAGAATGCC ACGGGTGACC TGGCCACCAG CAGGAATGCA GCGGATT	TCAC 246 TCAC 52 TCAC 249 T 63 TCCT 300 TCCT 277 TCCT 296 TCCT 102
R74593 corr. Consensus Translation R35464 N39798 H94519 R74593 corr.	ANTANTIACO TGACCAAGGA GGAGTGCCTC AAGAAATGTG CCACTGT AATAATTACO TGACCAAGGA GGAGTGCCTC AAGAAATGTG CCACTGT AATAATTACC TGACCAAGGA GGAGTGCCTC AAGAAATGTG CCACTGT AN N Y L T K E E C L K K C A T V AGAGAATGCC ACGGGTGACC TGGCCACCAG CAGGAATGCA GCGGATT	TCAC 246 TCAC 52 TCAC 249 T 65 TCCT 300 TCCT 217 TCCT 296 TCCT 132 TCCT 299
R74593 corr. Consensus Translation R35464 N39798 H94519	ANTANTIACO TGACCAAGGA GGAGTGCCTC AAGAAATGTG CCACTGT AATAATTACO TGACCAAGGA GGAGTGCCTC AAGAAATGTG CCACTGT AATAATTACC TGACCAAGGA GGAGTGCCTC AAGAAATGTG CCACTGT AN N Y L T K E E C L K K C A T V AGAGAATGCC ACGGGTGACC TGGCCACCAG CAGGAATGCA GCGGATT	TCAC 246 TCAC 52 TCAC 249 T 65 TCCT 300 TCCT 217 TCCT 296 TCCT 132 TCCT 299
R74593 corr. Consensus Translation R35464 N39798 H94519 R74593 corr. Consensus	ANTANTIACO TGACCAAGGA GGAGTGCCTC AAGAAATGTG CCACTGT AATAATTACO TGACCAAGGA GGAGTGCCTC AAGAAATGTG CCACTGT AATAATTACO TGACCAAGGA GGAGTGCCTC AAGAAATGTG CCACTGT N N Y L T K E E C L K K C A T V AGAGAATGCC ACGGGTGACC TGGCCACCAG CAGGAATGCA GCGGATT AGAGAATGCA ACGGGTGAC TGGCCACCAG CAGGAATGCA GCGGATGCA	TCAC 246 TCAC 52 TCAC 249 T 65 TCCT 300 TCCT 277 TCCT 296 TCCT 102 TCCT 299 S 3 32
R74593 corr. Consensus Translation R35464 N39798 H94519 R74593 corr. Consensus Translation	AATAATTACC TGACCAAGGA GGAGTGCCTC AAGAAATGTG CCACTGT N N Y L T K E E C L K K C A T V AGAGAATGCC ACGGGTGACC TGGCCACCAG CAGGAATGCA GCGGATT AGAGAATGCA ACGGGTGACC TGGCCACCAG CAGGAATGCA GCGGATT AGAGAATGCA ACGGGTGACA TGCAGAGATGCA GCGAGATGCA	TCAC 246 TCAC 52 TCAC 249 T 65 TCCT 300 TCCT 277 TCCT 296 TCCT 102 TCCT 102 TCCT 299 S 3 32 AGCGA 351
R74593 corr. Consensus Translation R35464 N39798 H94519 R74593 corr. Consensus	ANTANTIACO TGACCAAGGA GGAGTGCCTC AAGAAATGTG CCACTGT AATAATTACO TGACCAAGGA GGAGTGCCTC AAGAAATGTG CCACTGT AATAATTACO TGACCAAGGA GGAGTGCCTC AAGAAATGTG CCACTGT N N Y L T K E E C L K K C A T V AGAGAATGCC ACGGGTGACC TGGCCACCAG CAGGAATGCA GCGGATT CTGTCCCAAG TGCTCCCAGA AGGCAGGATT CTTGAAGACC ACTCCACCAG CTGTCCCAAG TGCTCCCAAG AGGCAGGATT CTTGAAGACC ACTCCACCAG CTGTCCCAAG TGCTCCCAAG AGGCAGGATT CTTGAAGACC ACTCCACCACCAG CAGGAGATC CTTGAAGACC ACTCCACCACCAG CAGGAGATC CTTGAAGACC ACTCCACCACCAG CAGGATT CTTGAAGACC ACTCCACCACCAG CAGGATT CTTGAAGACC ACTCCACCACCACCAG CAGGATT CTTGAAGACC ACTCCACCACCACCAG CAGGATT CTTGAAGACC ACTCCACCACCACCACCAG CAGGATT CTTGAAGACC ACTCCACCACCACCACCACCAG CAGGATT CTTGAAGACC ACTCCACCACCACCACCACCACCACCACCACCACCACCAC	TCAC 246 TCAC 52 TCAC 249 T 65 TCCT 300 TCCT 277 TCCT 296 TCCT 102 TCCT 102 TCCT 109 S 3 32 AGCGA 351 AGCGA 326
R74593 corr. Consensus Translation R35464 N39798 H94519 R74593 corr. Consensus Translation R35464 N39798	ANTANTIACO TGACCAAGGA GGAGTGCCTC AAGAAATGTG CCACTGT AATAATTACC TGACCAAGGA GGAGTGCCTC AAGAAATGTG CCACTGT AATAATTACC TGACCAAGGA GGAGTGCCTC AAGAAATGTG CCACTGT N N Y L T K E E C L K K C A T V AGAGAATGCC ACGGGTGACC TGGCCACCAG CAGGAATGCA GCGGATT AGAGAATGCC ACGGGTGACC TGGCCACCAG CAGGAATGCA GCGGAT CTGTCCCAAG TGCTCCCAGA AGGCAGGATT CTTGAAGACC ACTTCA	TCAC 246 TCAC 52 TCAC 249 T 65 TCCT 300 TCCT 277 TCCT 296 TCCT 102 TCCT 299 S 3 32 AGCGA 350 AGCGA 345
R74593 corr. Consensus Translation R35464 N39798 H94519 R74593 corr. Consensus Translation R35464 N39798 H94519	ANTANTIACO TGACCAAGGA GGAGTGCCTC AAGAAATGTG CCACTGT AATAATTACC TGACCAAGGA GGAGTGCCTC AAGAAATGTG CCACTGT AATAATTACC TGACCAAGGA GGAGTGCCTC AAGAAATGTG CCACTGT N N Y L T K E E C L K K C A T V AGAGAATGCC ACGGGTGACC TGGCCACCAG CAGGAATGCA GCGGATT CTGTCCCAAG TGCTCCCAGA AGGCAGGATT CTTGAAGACC ACTTCACCAG CTGTCCCAAG TGCTCCCAAG AGGCAGGATT CT-GAAGACC ACTTCACCAG CTGTCCCAAG TGCTCCCAAG AGGCAGGATT CT-GAAGACC ACTTCACCAG CTGTCCCAAG TGCTCCCAAGA AGGCAGGATT CT-GAAGACC ACTTCACCAG CTGTCCCAAG TGCTCCCAAGA AGGCAGGATT CT-GAAGACC ACTTCACCAG CTGTCCCAAG TGCTCCCAAGA AGGCAGGATT CT-GAAGACC ACTTCACCACCAG CTGTCCCAAG TGCTCCCAAGA AGGCAGGATT CT-GAAGACC ACTTCACCACACTCCAAGACC ACTTCCAAGACC ACTCCAAGACC AC	TCAC 246 TCAC 52 TCAC 249 T 65 TCCT 300 TCCT 277 TCCT 296 TCCT 102 TCCT 109 S 3 32 AGCGA 351 AGCGA 345 AGCGA 151
R74593 corr. Consensus Translation R35464 N39798 H94519 R74593 corr. Consensus Translation R35464 N39798 H94519 R74593 corr.	ANTANTIACO TGACCAAGGA GGAGTGCCTC AAGAANTGTG CCACTGT AATAATTACO TGACCAAGGA GGAGTGCCTC AAGAANTGTG CCACTGT AATAATTACO TGACCAAGGA GGAGTGCCTC AAGAANTGTG CCACTGT N N Y L T K E E C L K K C A T V AGAGAATGCC ACGGGTGACC TGGCCACCAG CAGGAATGCA GCGGATT CTGTCCCAAG TGCTCCCAGA AGGCAGGATT CTTGAAGACC ACTCCAC CTGTCCCAAG TGCTCCCAGA AGGCAGGATT CT-GAAGACC ACTCCACAC CTGTCCCAAG TGCTCCCAGA AGGCAGGATT CT-GAAGACC ACTCCACACACCACACCACACACCACACCACA	TCAC 246 TCAC 52 TCAC 249 T 65 TCCT 300 TCCT 277 TCCT 296 TCCT 102 TCCT 102 TCCT 299 S 3 32 AGCGA 351 AGCGA 345 AGCGA 346 AGCGA 346
R74593 corr. Consensus Translation R35464 N39798 H94519 R74593 corr. Consensus Translation R35464 N39798 H94519 R74593 corr. Consensus	ANTANTIACO TGACCAAGGA GGAGTGCCTC AAGAAATGTG CCACTGT AATAATTACO TGACCAAGGA GGAGTGCCTC AAGAAATGTG CCACTGT AATAATTACC TGACCAAGGA GGAGTGCCTC AAGAAATGTG CCACTGT N N Y L T K E E C L K K C A T V AGAGAATGCC ACGGGTGACC TGGCCACCAG CAGGAATGCA GCGGATT AGAGAATGCA ACGGGTGACC TGGCCACCAG CAGGAATGCA GCGGATT AGAGAATGCA ACGCAGGATT CTTGAAGACC ACTCCA CTGTCCCAAG TGCTCCCAGA AGGCAGGATT CTTGAAGACC ACTCCA	TCAC 246 TCAC 52 TCAC 249 T 65 TCCT 300 TCCT 277 TCCT 296 TCCT 102 TCCT 102 TCCT 299 S 3 32 AGCGA 351 AGCGA 345 AGCGA 346 AGCGA 346
R74593 corr. Consensus Translation R35464 N39798 H94519 R74593 corr. Consensus Translation R35464 N39798 H94519 R74593 corr.	ANTANTIACO TGACCAAGGA GGAGTGCCTC AAGAAATGTG CCACTGT AATAATTACC TGACCAAGGA GGAGTGCCTC AAGAAATGTG CCACTGT AATAATTACC TGACCAAGGA GGAGTGCCTC AAGAAATGTG CCACTGT N N Y L T K E E C L K K C A T V AGAGAATGCC ACGGGTGACC TGGCCACCAG CAGGAATGCA GCGGATT CTGTCCCAAG TGCTCCCAGA AGGCAGGATT CTTGAAGACC ACTCCAC CTGTCCCAAG TGCTCCCAAGA AGGCAGGATT CTTGAAGACC ACTCCACCAC CTGTCCCAAG TGCTCCCAAGA AGGCAGGATT CTTGAAGACC ACTCCACCACCACCACCACCACCACCACCACCACCACCAC	TCAC 246 TCAC 52 TCAC 249 T 65 TCCT 300 TCCT 217 TCCT 296 TCCT 132 TCCT 132 TCCT 299 S 3 32 AGCGA 351 AGCGA 345 AGCGA 345 AGCGA 346 AGCGA 346 AGCGA 346 AGCGA 346 AGCGA 346
R74593 corr. Consensus Translation R35464 N39798 H94519 R74593 corr. Consensus Translation R35464 N39798 H94519 R74593 corr. Consensus Translation	ANTANTIACO TGACCAAGGA GGAGTGCCTC AAGAAATGTG CCACTGT AATAATTACO TGACCAAGGA GGAGTGCCTC AAGAAATGTG CCACTGT AATAATTACC TGACCAAGGA GGAGTGCCTC AAGAAATGTG CCACTGT AATAATTACC TGACCAAGGA GGAGTGCCTC AAGAAATGTG CCACTGT N N Y L T K E E C L K K C A T V AGAGAATGCC ACGGGTGACC TGGCCACCAG CAGGAATGCA GCGGATT AGAGAATGCC ACGGGTGACC TGGCCACCAG CAGGAATGCA GCGGGATT AGAGAATGCC ACGGGTGACC TGGCCACCAG CAGGAATGCA GCGGGATT AGAGAATGCC ACGGGTGACC TGGCCACCAG CAGGAATGCA GCGGGATT CTGTCCCAAG TGCTCCCAAGA AGGCAGGATT CT-GAAGACC ACTCCAC CTGTCCCAAG TGCTCCCAAGA AGGCAGGATT CT-GAAGACC ACTCCAC CTGTCCCAAG TGCTCCCCAGA AGGCAGGATT CT-GAAGACC ACTCCAC CTGTCCCAAG TGCTCCCAAGA AGGCAGGATT CT-GAAGACC ACTCCAC CTGTCCCAAG TGCTCCCCAGA AGGCAGGATT CT-GAAGACC ACTCCAC CTGTCCCAAG TGCTCCCCAGA AGGCAGGATT CT-GAAGACC ACTCCACC CTGTCCCAAG TGCTCCCCAGA AGGCAGGATT CT-GAAGACC ACTCCACC CTGTCCCAAG TGCTCCCCAGA AGGCAGGATT CT-GAAGACC ACTCCACCACC CTGTCCCAAG TGCTCCCCAGA AGGCAGGATT CT-GAAGACC ACTCCACCACCACCACCACACCACACACCACAC	TCAC 246 TCAC 52 TCAC 249 T 65 TCCT 300 TCCT 277 TCCT 296 TCCT 102 TCCT 102 TCCT 299 S 3 32 AGCGA 345 AGCGA 345 AGCGA 346 AGCGA 348 S D 99
R74593 corr. Consensus Translation R35464 N39798 H94519 R74593 corr. Consensus Translation R35464 N39798 H94519 R74593 corr. Consensus Translation R35464 R39798 R94519 R74593 corr. Consensus Translation	ANTANTIACO TGACCAAGGA GGAGTGCCTC AAGAAATGTG CCACTGT AATAATTACO TGACCAAGGA GGAGTGCCTC AAGAAATGTG CCACTGT AATAATTACC TGACCAAGGA GGAGTGCCTC AAGAAATGTG CCACTGT AATAATTACC TGACCAAGGA GGAGTGCCTC AAGAAATGTG CCACTGT N N Y L T K E E C L K K C A T V AGAGAATGCC ACGGGTGACC TGGCCACCAG CAGGAATGCA GCGGATT AGAGAATGCC ACGGGTGACC TGGCCACCAG CAGGAATGCA GCGGGATT AGAGAATGCC ACGGGTGACC TGGCCACCAG CAGGAATGCA GCGGATT CTGTCCCAAG TGCTCCCAGA AGGCAGGATT CT-GAAGACC ACTCCAC CTGTCCCAAG TGCTCCCAGA AGGCAGGATT CT-GAAGACC ACTCCACCAC CTGTCCCAAG TGCTCCCAGA AGGCAGGATT CT-GAAGACC ACTCCACCACAC CTGTCCCAAG TGCTCCCAGA AGGCAGGATT CT-GAAGACC ACTCCACCACACACACACACACACACACACACACAC	TCAC 246 TCAC 52 TCAC 249 T 65 TCAC 249 T 65 TCCT 300 TCCT 277 TCCT 296 TCCT 299 S 3 32 AGCGA 352 AGCGA 346 AGCGA 346 S D 99 CTGGG 372
R74593 corr. Consensus Translation R35464 N39798 H94519 R74593 corr. Consensus Translation R35464 N39798 H94519 R74593 corr. Consensus Translation R35464 N39798	ANTANTIACO TGACCAAGGA GGAGTGCCTC AAGAAATGTG CCACTGT AATAATTACO TGACCAAGGA GGAGTGCCTC AAGAAATGTG CCACTGT AATAATTACO TGACCAAGGA GGAGTGCCTC AAGAAATGTG CCACTGT AATAATTACO TGACCAAGGA GGAGTGCCTC AAGAAATGTG CCACTGT N N Y L T K E E C L K K C A T V AGAGAATGCC ACGGGTGACC TGGCCACCAG CAGGAATGCA GCGGATT CTGTCCCAAG TGCTCCCAGA AGGCAGGATT CT-GAAGACC ACTCCAC CTGTCCCAAG TGCTCCCAGA AGGCAGGATT CT-GAAGACC ACTCCACCAC TATGTT-CAA CTA-TG-AAG AATAATTGCA CCGNCAACGA ATTCACCACACACACACACACACACACACACACACACA	TCAC 246 TCAC 52 TCAC 249 T 65 TCAC 249 T 65 TCAC 277 TCCT 277 TCCT 296 TCCT 299 S 3 32 AGCGA 351 AGCGA 345 AGCGA 345 AGCGA 346 S D 99 CTGGG 372 CTGGG 392
R74593 corr. Consensus Translation R35464 N39798 H94519 R74593 corr. Consensus Translation R35464 N39798 H94519 R74593 corr. Consensus Translation R35464 N39798 H94519 R35464 N39798 H94519	ANTANTIACO TGACCAAGGA GGAGTGCCTC AAGAAATGTG CCACTGT AATAATTACO TGACCAAGGA GGAGTGCCTC AAGAAATGTG CCACTGT AATAATTACO TGACCAAGGA GGAGTGCCTC AAGAAATGTG CCACTGT AATAATTACO TGACCAAGGA GGAGTGCCTC AAGAAATGTG CCACTGT N N Y L T K E E C L K K C A T V AGAGAATGCC ACGGGTGACC TGGCCACCAG CAGGAATGCA GCGGAT CTGTCCCAAG TGCTCCCAGA AGGCAGGATT CTTGAAGACC ACTCCA CTGTCCCAAG TGCTCCCAGA AGGCAGGATT CT-GAAGACC ACTCCA CTGTCCCAAG TGCTCCAAGA AATACT-GCA CCGCCAACGC AGTCAC TATGTT-CAA CTA-TG-AAG AATACT-GCA CCGCCAACGC AGTCAC TATGTT-CAA CTA-TG-AAG AATACT-GCA CCGCCAACGC AGTCAC TATGTT-CAA CTA-TG-AAG AATACT-GCA CCGCCAACGC AGTCAC	TCAC 246 TCAC 52 TCAC 249 T 65 TCAC 249 T 65 TCAC 277 TCAC 277 TCAC 277 TCAC 277 TCAC 300 TCA
R74593 corr. Consensus Translation R35464 N39798 H94519 R74593 corr. Consensus Translation R35464 N39798 H94519 R74593 corr. Consensus Translation R35464 N39798 H94519 R74593 corr.	AATAATTACC TGACCAAGGA GGAGTGCCTC AAGAAATGTG CCACTGT AATAATTACC TGACCAAGGA GGAGTGCCTC AAGAAATGTG CCACTGT AATAATTACC TGACCAAGGA GGAGTGCCTC AAGAAATGTG CCACTGT N N Y L T K E E C L K K C A T V AGAGAATGCC ACGGGTGACC TGGCCACCAG CAGGAATGCA GCGGAT CTGTCCCAAG TGCTCCCAGA AGGCAGGATT CTTGAAGACC ACTCCA CTGTCCCAAG TGCTCCCAGAA AGGCAGGATT CTTGAAGACC ACTCCA CTGTCCCAAG TGCTCCCAAGA AATACTTGCA CCGCCAACGC AGTCAC CTGTCCCAAA CTA-TG-AAG AATACTTGCA CCGCCAACGC AGTCAC CTATGTT-CAA CTA-TG-AAG AATACTTGCA CCGCCAACGC AGTCAC	TCAC 246 TCAC 52 TCAC 249 T 65 TCAC 249 T 65 TCAC 277 TCAC 277 TCAC 277 TCAC 277 TCAC 279 S 3 32 AGCGA 351 AGCGA 326 AGCGA 345 AGCGA 346
R74593 corr. Consensus Translation R35464 N39798 H94519 R74593 corr. Consensus Translation R35464 N39798 H94519 R74593 corr. Consensus Translation R35464 N39798 H94519 R35464 N39798 H94519	AATAATTACC TGACCAAGGA GGAGTGCCTC AAGAAATGTG CCACTGT AATAATTACC TGACCAAGGA GGAGTGCCTC AAGAAATGTG CCACTGT AATAATTACC TGACCAAGGA GGAGTGCCTC AAGAAATGTG CCACTGT N N Y L T K E E C L K K C A T V AGAGAATGCC ACGGGTGACC TGGCCACCAG CAGGAATGCA GCGGATT AGAGAATGCC ACGGGTGACC TGGCCACCAG CAGGAATGCA GCGGAT CTGTCCCAAG TGCTCCCAGA AGGCAGGATT CTTGAAGACC ACTCCA CTGTTCCCAAG TGCTCCCAGA AGGCAGGATT CTTGAAGACC ACTCCA CTGTCCCAAG TGCTCCCAGA AGGCAGGATT CTTGAAGACC ACTCCA CTGTTCCCAAG TGCTCCCAGA AATAATTGCA CCGCCAACGC AGTCAC TATGTT-CAA CTA-TG-AAG AATACT-GCA CCGCCAACGC AGTCAC	TCAC 246 TCAC 52 TCAC 249 T 65 TCAC 249 T 65 TCAC 277 TCAC 277 TCAC 277 TCAC 277 TCAC 279 S 3 32 AGCGA 351 AGCGA 326 AGCGA 345 AGCGA 346

R35464		
N39798	CCTTGC-GTG GAATCCTTTC CCACGCTGGN AATTTNGACG TTGAGAAGGA 421	
H94519	CCT-GC-GTG -CATCCTT-C CCACGCTGGT ACTTT-GNCG 427	
R74593 corr.	CCTTGCCGTG -CATCCTT-C CCACGCTGGT ACTTT-GACG TGGAGA-GGA 243	
Consensus	COTTGCCJTG -CATCCTT-C CCACGCTGGT ACTTT-GACG TGGAGA-GGA 440	
Translation	PCRASE PRWY F D V ER N 129	
R35464		
N39798	AC 423	
H94519		
R74593 corr.	ACTCCTGCAA TAACTTCATC TATGGAGGCT GCCGGGGCAA TAAGAACAGC 293	
Consensus	ACTOCTGCAA TAACTTCATO TATGGAGGOT GOOGGGGCAA TAAGAACAGO 490	
Translation	SCN NEI Y G G C R G N K N S 145	
R35464		
N39798		
H94519		
R74593 corr.	TACCGCTCTG AGGAGGCCTG CATGCTCCGC TGCTTCCGCC AGCAGGAGAA 343	
Consensus	TACCGCTCTG AGGAGGCCTG CATGCTCCGC TGCTTCCGCC AGCAGGAGAA 540	
Translation	YRSEEACHLRCFRQ QEN 162	
	•	
R35464		
N39798		
H94519		
R74593 corr.	TOCTOCCOTG COCCTTGGCT CAMAGGTGGT GGTTCTGGCC GGGGCTGTTT 393	
Consensus	TOCTOCCOTG COCCTTGGCT CANAGGTGGT GGTTCTGGCC GGGGCTGTTT 590	
Translation	PPLPLGS KVV V LAGAV 5179	
R35464		
N39798		
H94519		
R74593 corr.	CGTGATGGTG TTGATCCTTT TCCTGGGGAG CNTCCATGGT CTTACTGATT 443	
Consensus	CGTGATGGTG TTGATCCTTT TCCTGGGGAG CNTCCATGGT CTTACTGATT 640	
Translation	• W C • S F S W G A S M V L L I 195	
R35464	***************************************	
N39798		
H94519		
R74593 corr.		
Consensus	CCGGGTGGCA AGGAGGAACC AGGAGCGTGC CCTGCGGANC_GTCTGGAGCT 690	
Translation	PGGKEEPGACPA R LE L III	
R35464	***************************************	
N39798		
H94519		
R74593 corr.	TCGGAGATGA CAAGGGNT 511	
Consensus	TOGGAGATGA CAAGGGNT	
	R R * Q G	
Translation	K K - Q U	
VEV		
KEY	eic acid sequence of EST R35464 (SEQ ID NO.: 12)	
N30300 = NUCLO	ers acid sequence of EST N39798 (SEQ ID NO.: 17)	
	ers acid sequence of EST H94519 (SEQ 15 NO : 17)	

H94519 - Nucleic acid sequence of EST H94519 (SEQ ID NO.: 16) R74593 corr - Correct d version of (SEQ ID NO.: 14) G at b.p. 114 Consensus - Nucelic acid sequence for numan bikunin (SEQ ID NO.: 3) Translation - Amino acid Translation of Consensus (SEQ ID NO.: 13) Schematic depicting the overlap of ESTs bearing homology to the cDNA sequence encoding placental bikunin



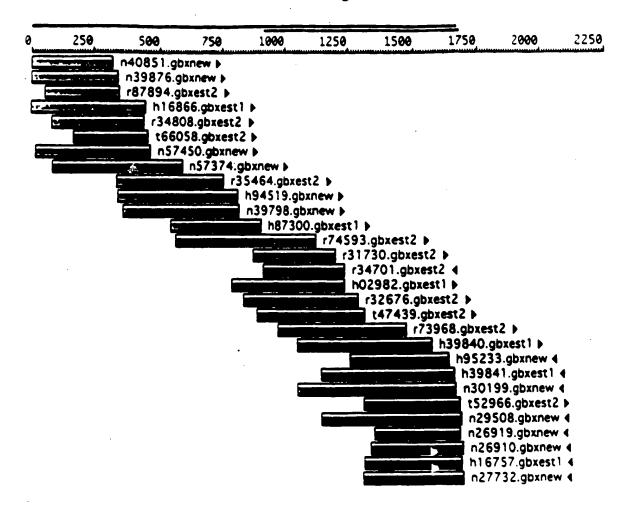


Figure 4C

	:				50
Bikunin	scga	cotoccccs	TTGGGAGGTG	TAGCGCGGCT	CTGAACGCGT
N4085:	GCSA	cetecces	TTGGGAGGTG	TAGCGCGGCT	CTGAACGCGT
N39876		cereceses	TTGGGAGGTG	TAGCGCGGCT	CTGAACGCGT
R87894					
H16866	GGCGA	cctcccccc	TTGGGAGGTG	TAGCGCG.CT	CTGANCGGGN
R34838					
766058					
N57450	• • • • • • • • • • • • • • • • • • • •			TAGCGCGGCT	CTGAACGCNA
N57374					
R35464	• • • • • • • • • • • • • • • • • • • •				
H94519					
N39798					
H67300					
R74593					
R31730					
R34701					
802982			· · · · · · · · · · · · · · · ·		
R32676	• • • • • • • • • • • • • • • • • • • •				
747439					
R73968	• • • • • • • • • • •				
H39840	• • • • • • • • • •				
95233	• • • • • • • • • • •				
E39841	• • • • • • • • • • • • •				
N30199	• • • • • • • • • • • • • • • • • • • •				
752966	• • • • • • • • • • • • • • • • • • • •				
N29508					
N26919					
N26910	• • • • • • • • • • • • • • • • • • • •				
H: 6757					
427777					

	51	,000	•		120
Bikunin	GNA GGGCCG	TTGAGTGTCG	CAGGCGGCGA	GGGCGCGAGT	GAGGAGCAGA
N4085:	NGAGNGGCCG			GGGCGCGAGT	
N39876	SCA. GSGCCG			SSSCSCSAST	
987894				SGGCGCSAGT	
H16866	ANGGGCCG			GGGCN.GAGT	
R34808					
166058					
NS7450	GAAGNGGCCG			GGGCGCGAGT	
N57374					
R35464					
H94519					
N39798					
H87300					
R74593					• • • • • • • • • •
R31730					
R34701			· · · · · · · · · · · · · · · ·		• • • • • • • • • •
HC2982	• • • • • • • • • • • • • • • • • • • •				
R32676	• • • • • • • • • • • • • • • • • • • •				
747439			· · · · · · · · · · · · · · · ·		
273968					
H39840					
H95233	• • • • • • • • • • • • • • • • • • • •				
H39841	• • • • • • • • • • • • • • • • • • • •	• • • • • • • • • • •			
N30199	••••••				
752966	• • • • • • • • • •	• • • • • • • • • • • • • • • • • • • •			
N29508	• • • • • • • • • • • • • • • • • • • •				
N26919	• • • • • • • • • • • • • • • • • • • •				
N26910	• • • • • • • • • • • • • • • • • • • •	• • • • • • • • •			
H16757	• • • • • • • • • • • • • • • • • • • •				
N27732					

N26919

N26910

H: 6757

Figure 4C (C n't) :01 :50 BIRRHIA CCCAGGCATC GCGCGCCGAG AAGNC GGGC GTCCCCACAC TGAAGGTCCG N40851 CCCAGGCATC GCGCGCCGAG AAGNC.GGGC GTCCCCACAC TGAAGGTCCG N39876 CCCAGGCATC GCGCGCCGAG AAGNC.GGGC NTCCCCACAC TGAAGGTCCG R87894 CCCAGGCATE GESEGEEGAG AAGGEESSGE GTECCEACAE TSAAGGTEES H16866 CCCAGGCATC GCGCGCCGAG AAGNC.GGGC GTCCCCACAC TGAAGGTCCG CCCAGGCATC GCGCGCCGAG AAGNC.GGGC GTCCCCACAC TGAAGGTCCG 166058 N57450 CCCAGGCATC GCGCGCCGAG AAGNC.GGGC GTCCCCACAC TGAAGGTCCG CCCAGGCATC GCGCGCCGAG AAGNC.GGGC GTCCCCACAC TGAAGGTCCG R35464 H94519 N39798 H87300 R74593 R31730 R3470: HC2982 232676 747439 R73968 H39840 H95233 H39841 N30199 N29508

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gure 40	: (Con't)		
151				200
GAAAGSCSA	c	TTTGGCACCT	GGCGGACCCT	CCCGGAGCGT
GAAAGGCGA	- 110066666	TTTGGCACCT	GGCGGACCCT	CCCGGAGCGT
GAAAGGCGA	TTCCGGGGGC	TTTGGCACCT	GGCGGACG.T	CCCGGAGCN.
GAAAGGCGA	TTCCGGGGCC	TTTGGCACCT	GGCGGACCCT	CCCGGAGCGT
GAAAGGCGAG	222222211	TTTGGCACCT		
GAMAGGCGAG	: :::::::::::::::::::::::::::::::::::::	TTTGGCACCT	GGCGGACCCT	CCCGGAGCGT
• • • • • • • • • • • •				
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• • • • • • • • • • • • • • • • • • • •	• • • • • • • • • • • • • • • • • • • •	• • • • • • • • • •		• • • • • • • • • • • • • • • • • • • •
	15: GAAAGGCGA: GAAAGGCGA: GAAAGGCGA: GAAAGGCGA: GAAAGGCGA: GAAAGGCGA: GAAAGGCGA:	SE GAMAGGCGAC TECCGGGGGC	GAAAGGCGAC TTCCGGGGGC TTTGGCACCT	GAAAGGCGAC TTCCGGGGGC TTTGGCACCT GGCGGACCCT GAAAGGCGAC TTCCGGGGGC TTTGGCACCT GGCGGACCCT COMMAN C

	20:	•			250
Bikunin	CGSCACCTSA	ACGCGAGGCG	CTCCATTGCG	CSTGCSTTTG	. AGGGGCTTC
N4085:	COSCACCISA	ACGCGAGGCG	CTCCATTGCG	CSTGCSTNTG	. AGGGGCTTC
N39876	CGSCACCTGA	ACGCGAGGCG	CTCCATTGCG	CGTGCGTTTG	. AGGGGCTTC
R87894	COGCACCTGA	ACSCSAGGCS	CTCCATTGCS	CGTGCGTTTG	. AGGGGCTTC
H16866	.GGCACCTGA	ACGCGAGGCG	CTCCATTGCG	CSTGCSTTTG	. AGGGGCTTC
R34808	CGGCACCTGA	ACCCGAGGCG	CTCCATTGCG	CGTGCSTNTG	GAGGGGCTTC
766058	CGGCACCTGA	ACCCGAGGE.	CTCCATTGCS	.GTGCGTGTG	MAGGCSCTTC
N57450	CGGCACCTGA	ACGCGAGGCG	CTCCATTGCG	CGTGCGTTTG	. AGGGGCTTC
N57374	COGCACCTGA	ACGCGAGGC.	CTCCATTGC.	CGTGCGTTNG	. AGGGGCTTC
R35464					
H94519					
N39798					
H87300					
R74593					
R31730					
R34701			• • • • • • • • • • •		
HC2982					
R32676		• • • • • • • • • • • • • • • • • • • •			
747439					
373968	• • • • • • • • • • • • • • • • • • • •				
839840					
H95233					
H3984:	• • • • • • • • • • • • • • • • • • • •				
N3C199					
752966					
N29508			• • • • • • • • • • • • • • • • • • • •		
N26919					
N26910					
H16757					
N27732					

	251				300
Bikunin	CCGCACCT G	ATCGCGAGAC	CCCAACGGCT	SGTGG CSTC	ac to cata
N40851	CCGCACCT.G	ATCGCGAGAC	CCCAACSSCT	GGTGG.CGTC	accta.caci
N39876	CCGCACCT.G	ATCGCGAGAC	CCCAACGGCT	SGTGG.CSTC	50000.0000
987994	CCSCACCT.S	ATCGCGAGAC	CCCAACGGCT	GCTNG.CGTC	GC.TN.CGCS
H16866	CCGCACCT.G	ATCGCGAGAC	CCCAACGGCT	GGTNG.CGTC	GC.TGGCGCS
234808	CCGCACCT.G	ATCCCGAGAC	CCCAACGGCT	GGTGGGCGTT	GC . TG . 1.605
166058	CCGCACCT.G	ATCGCGAGAC	CCCAACGGCT	GGTGG.CGTC	GC.TG.CGCG
N57450	CCGCACCT.G	ATCSCGAGAC	CCCAACGGCT	SGTGG.CSTC	cccts.cccs
N57374	CCGGAACTTS	ATCGCGAGAC	CCCAACGGCT	GGTGG.CGTC	GC.TS.CGCS
R35464					
H94519					
N39798					
H87300					
A74593	• • • • • • • • • • • • • • • • • • • •				
R31730					
R34701	• • • • • • • • • • • • • • • • • • • •				
H02982	• • • • • • • • • • • • • • • • • • • •				
R32676					
747439	• • • • • • • • • • • • • • • • • • • •				
P13968					
H39840	• • • • • • • • • • • • • • • • • • • •				
H95233					
H3984:					
N30199					
752966			· · · · · · · · · · · · ·		
N29508					
N26919					
N26910					
H16757		· · · · · · · · · · · · · · · ·	• • • • • • • • • • • • • • • • • • • •		
N27732					

N26910

H16757

M27732

(Con't) Figure 40 30: TO TOUGHTS AGET GUICA TUUCGCANT GTTUG GUGG T GAGGE GG Bikunin N40851 TO TOGGETS AGET GENCA TETCS N39876 TC.TCGGCTG AGCT.GGCCA TGGCGCACT. G.TGCGGNGC T.GAGGC.G TO. TOGGETG AGETTGGECA TGGCGCANT. GTTNC.GGGC T.NAGGC.GG TTCTCGGCTG AGCT.GGCCA TGGCGCANT. GTTGC.GNGC T.GAGGC.GG R348C8 TOTTOGGOTG AGCTGGGCCA TGGCGCANTT GTTGC.GGGC T.GAGGC.GG 766058 TO TOSSETS AGET. GGECA TGGCGCANT, GTTGC. GNGC T. GAGGC. GG N57450 TO TOGGETS AGCT. GGCCA TGGCGCANT. GGTGC. GGGC TTGAGGC.GG N57374 TOOTOGGOTG AGCT.GGCCA TGGCGCANT. GGTGCCGNGC T.GAGGCCGG R35464 H94519 N39798 H87300 R74593 331730 33470: 802962 R32676 747439 R73968 H95233 *********** H3984: N30199 752966 N29508 N26919

416757

Figure 4C (Con't) 400 Bikunin AC SG CS TITCICS CO TOCTOGO A TOGOT OF T COTOTOT R87894 ACG. H16866 AC...CONCCT TITTETTES. COTTGGTGGG ATTGGCTTGG TTGGTNTCTG 214808 ACGCGGNCG. .TTTTTTCGN CCTTGCTGGG ATTLULITS. IINCTCTCTN ... CGGNCG. .TTTTCTCG. CC.TGCTGGG A.TCGCT.GC T.CCTCTCT. N57450 ANNINGCEG. .. TITTETEG. CO. TOCTOGG A. TOGET. GC T. CETETET. N57374 AG...GGCCGG ...TTTCTCG. CCTTGCTGGG A.TCGCT.GC T.CCTCTCTGGTCG. ..TTTCTCG. CCTGGCTGGG A.TCGCT.GC T.CCTCTCT. H94519 .GCNGCGCG. ..TTNNTCG. CN.IGCTGGG A.TCGCT.GC A.CCTCTCT. N39798CTGGG ANTCGCT.GC T.CCTCTCT. **K87300** R74593 R3:730 R34701 HO2982 932676 747439 R73968 H39840 H95233 R39841 N3C139 752966 N29508 N26919 N26910

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, li	gure	4C	(Con't)		
	401					450
Bikunin	GGGG :	cets (COCCCGA	CCGA GAACG	CA GCA TCC	
H:6866	GGGCTT	cers (G. CGGCCSA	CCGA . GAACG	CA.GCA.TCC	AACAATTTT
R34808	SCCCTT	c. ts (GGNGGCCGA	NCGA . SAACS	CAAGCA TTC	ACCA
766058	GGGS . T:	=======================================	CSGCCSA	CEGA . SAACG	CA.GCA.TCC	ACCANTS CT
N57450	SSCS . T:	::::: (CGGCCGA	CCGA GAACG	CA.GCA.TCC	ACCACTE CT
N\$7374	- GGGG . TO	eets c	CSGCCGA	NCGAAGAANG	CA.SCAATCC	ANCAL STUCE
R35464	SGGG. TO	CTG C	. CCGGCCGA	CCGA . GAACG	CA.GCA.TCC	ACCACTT CT
H94519	GGGG. TO	CNG G	CGGCCGA	CCGA GAACG	CA.GCA.TCC	ACCACES CO
N39798	GGGG. TO	crc c	CGGCCGA	CCGA . GAACG	CA.GCA.TCC	ACCACT CT
H87300						ncunc
R74593						• • • • • • • • • • • • • • • • • • • •
R3:730			• • • • • • • • •			
R34701						
H02982						
R32676						
747439						• • • • • • • • • • • • • • • • • • • •
R73968					• • • • • • • • • • • • • • • • • • • •	
H3984C						
H95233						• • • • • • • • • • • • • • • • • • • •
H39841			-		• • • • • • • • • • • • • • • • • • • •	
N30199			•			• • • • • • • • • • • • • • • • • • • •
752966						• • • • • • • • • •
N29508						• • • • • • • • • • • • • • • • • • • •
N26919						• • • • • • • • • • • • • • • • • • • •
N26910					• • • • • • • • • • • • • • • • • • • •	• • • • • • • • • • • • • • • • • • • •
H16757	• • • • • • • •					• • • • • • • • • • •
N27732					• • • • • • • • • • • •	• • • • • • • • • • • • • • • • • • • •

	451				500
Bikunin	GCCTGGTGT	CSAAGST SS	TOGGEAGATS		CATGCCTA S
H16866	SCC				
766058	TCCTGGTGTT	CGAAGG			
N57450	GCCTGGTGT,	CGAAGST.SS	TOGGCAG		
857374	SCCTGGTSTT	CGAAAGTTSS	TEGECANATT	0000000011	CATGNCTAAS
R35464	GCCTGGTGT.	CGAAGGT . SC			
h94519	GCCTGSTST.	CGAAGGT . SG	TGGGCAGATG	CCGGG.CCTC	CATGCCTA.G
H39798	GCCTGGTGT.	CGAAGGT . SG	TGGGCAGATG	ccccc.cctc	CATGCCTA.G
H87300					
R74593					
831730	• • • • • • • • • • • • • • • • • • • •				
334701					
H02982	• • • • • • • • • • • • • • • • • • • •				
R32676	• • • • • • • • • • • • • • • • • • • •				
747439					
373968					
#3984C					
H95233	• • • • • • • • • • • • • • • • • • • •				
839041	• • • • • • • • • • • • • • • • • • • •				
N30199	• • • • • • • • • • •				
752966	• • • • • • • • • • • • • • • • • • • •				
N29508	• • • • • • • • • • • • • • • • • • • •				
N26919		• • • • • • • • • • • • • • • • • • • •			
N26910	• • • • • • • • • • • •				
H16757	• • • • • • • • • • • • • • • • • • • •			• • • • • • • • • • • •	
N27732		· • • • • • • · · ·			

Fi	gure 40	(Con't)		
	501				550
Bikunin	S TOST GG	ACANTOTOAC	TGACGGATCC	TOCCAGOTOT	TESTOT ATS
N57374	GTTGGTTGG	ANAATGTNAA	TTAANGATTO	TTGCAACTGT	TISTGINATE
R35464	G.TGGT.GG	ACANTGTOAC	TGACGGATCC	TGCCAGCTGT	TTSTGT.ATS
H94519	S. TSST. GS	ACAATGTCAC	TOACGGATCE	TECTAGCTET	TTSTST.ATS
N39798	G. TGST.GS	ACANTGTONO	TGACGGATCC	TGCCAGCTGT	TIGTGT.ATG
H87300	• • • • • • • • • • •				
R74593					
R31730					
R347C:	• • • • • • • • • •				
H02982	• • • • • • • • • • • •				
R32676	• • • • • • • • • • •			• • • • • • • • • • • • • • • • • • • •	
747439	• • • • • • • • • •	• • • • • • • • • • • • • • • • • • • •	• • • • • • • • • • • • • • • • • • • •		• • • • • • • • •
R73968	• • • • • • • • • • • • • • • • • • • •				
H3984C					
H95233	• • • • • • • • • • • • • • • • • • • •	• • • • • • • • • • • • • • • • • • • •			
239841			• • • • • • • • • • • • • • • • • • • •		
N30199					
752966	• • • • • • • • • • • • • • • • • • • •	• • • • • • • • • • • • • • • • • • • •	• • • • • • • • • • • • • • • • • • • •		
N29508	• • • • • • • • • • • • • • • • • • • •	• • • • • • • • • • • • • • • • • • • •	• • • • • • • • • • • • • • • • • • • •		
N26919	• • • • • • • • • • • • • • • • • • • •	• • • • • • • • • • • • • • • • • • • •	• • • • • • • • • • •	· · · · · · · · · · · · · · · · · · ·	
N2691C	• • • • • • • • • • • • • • • • • • • •		• • • • • • • • • • • • • • • • • • • •	· · · · · · · · · · · · · · · · · · ·	
H16757	• • • • • • • • • • • • • • • • • • • •		• • • • • • • • • • • • • • • • • • • •	· • • • • • • • • • • • • • • • • • • •	
N27732	• • • • • • • • • • •				
				••••••	•••••
	551				600
BIKUNIA	SSSGCTSTGA			CCTGACCAAG	GA GGAGTGC
N57374	GGGGCTGTGA GGGGCTNTTA	AACGGAAANA	. CAATAATNA	CCTGACCAAG CCTGACCAAA	GA GGAGTGC GAAGNAAT
N5"374 R35464	GGGGCTGTGA GGGGCTNTTA GGGGCTGTGA	AACGGAAANA CGGAAACA	.CAATAATNA GCAATAATTA	CCTGACCAAG CCTGACCAAA CCTGACCAAG	GA GGAGTGC GAAGNAAT GA.GGAGTGC
N5°374 R35464 H94519	CGGGCTGTGA CGGGCTNTTA CGGGCTGTGA CGGGCTGTGA	AACGGAAANA CGGAAACA CGGAAACA	.CAATAATNA GCAATAATTA GCAATAATTA	CCTGACCAAG CCTGACCAAA CCTGACCAAG CCTGACCAAG	GA GGAGTGC GAAGNAAT GA.GGAGTGC GA.GGAGTGC
N57374 R35464 H94519 N39798	GGGGCTGTGA GGGGCTNTTA GGGGCTGTGA GGGGCTGTGA GGGGCTGTGA	AACGGAAANA CGGAAACA CGGAAACA	.CAATAATHA GCAATAATTA GCAATAATTA GCAATAATTA	CCTGACCAAG CCTGACCAAG CCTGACCAAG CCTGACCAAG	GA GGAGTGC GAAGNAAT GA.GGAGTGC GA.GGAGTGC GA.GGAGTGC
N57374 R35464 H94519 N39798 H8730C	GGGGCTGTGA GGGGCTNTTA GGGGCTGTGA GGGGCTGTGA GATTCGGCAC	AACGGAAACACGGAAACACGGAAACACGGAAACA AGGGGAAACA	.CAATAATHA GCAATAATTA GCAATAATTA GCAATAATTA GCAATAATTA	CCTGACCAAG CCTGACCAAA CCTGACCAAG CCTGACCAAG CCTGACCAAG	GA GGAGTGC GAAGNAAT GA.GGAGTGC GA.GGAGTGC GA.GGAGTGC GA.GGAGTGC
N57374 R35464 H94519 N39798 H8730C R74593	GGGGCTGTGA GGGGCTNTTA GGGGCTGTGA GGGGCTGTGA GGGGCTGTGA	AACGGAAANA CGGAAACA CGGAAACA	CAATAATNA GCAATAATTA GCAATAATTA GCAATAATTA GCAATAATTA	CCTGACCAAG CCTGACCAAG CCTGACCAAG CCTGACCAAG	GA GGAGTGC GAAGNAAT GA.GGAGTGC GA.GGAGTGC GA.GGAGTGC
N57374 R35464 H94519 N39798 H8730C	GGGGCTGTGA GGGGCTNTTA GGGGCTGTGA GGGGCTGTGA GATTCGGCAC	AACGGAAACACGGAAACACGGAAACACGGAAACA AGGGGAAACA	CAATAATNA GCAATAATTA GCAATAATTA GCAATAATTA GCAATAATTA GCAATAATTA	CCTGACCAAG CCTGACCAAA CCTGACCAAG CCTGACCAAG CCTGACCAAG	GA GGAGTGC GAAGNAAT GA.GGAGTGC GA.GGAGTGC GA.GGAGTGC GA.GGAGTGC
N57374 R35464 H94519 N39798 H8730C R74593 R3173C R34701	GGGGCTGTGA GGGGCTNTTA GGGGCTGTGA GGGGCTGTGA GATTCGGCAC	AACGGAAACACGGAAACACGGAAACACGGAAACA AGGGGAAACA	CAATAATNA GCAATAATTA GCAATAATTA GCAATAATTA GCAATAATTA	CCTGACCAAG CCTGACCAAG CCTGACCAAG CCTGACCAAG CCTGACCAAG CCTGACCAAG	GA GGAGTGC GAAGNAAT GA.GGAGTGC GA.GGAGTGC GA.GGAGTGC GA.GGAGTGC
N57374 R35464 H94519 N39798 H8730C R74593 R3173C R34701 H02982	GGGGCTGTGA GGGGCTGTGA GGGGCTGTGA GGGGCTGTGA GATTCGGCAC	AACGGAAACACGGAAACACGGAAACACGGAAACA AGGGGAAACA	CAATAATNA GCAATAATTA GCAATAATTA GCAATAATTA GCAATAATTA GCAATAATTA	CCTGACCAAG CCTGACCAAG CCTGACCAAG CCTGACCAAG CCTGACCAAG CCTGACCAAG	GA GGAGTGC GAAGNAAT GA.GGAGTGC GA.GGAGTGC GA.GGAGTGC GA.GGAGTGC
N57374 R35464 H94519 N39798 H8730C R74593 R3173C R34701	GGGGCTGTGA GGGGCTGTGA GGGGCTGTGA GGGGCTGTGA GATTCGGCAC	AACGGAAACACGGAAACACGGAAACACGGAAACA AGGGGAAACA	CAATAATNA GCAATAATTA GCAATAATTA GCAATAATTA GCAATAATTA GCAATAATTA	CCTGACCAAG CCTGACCAAG CCTGACCAAG CCTGACCAAG CCTGACCAAG CCTGACCAAG	GA GGAGTGC GAAGNAAT GA.GGAGTGC GA.GGAGTGC GA.GGAGTGC GA.GGAGTGC
N57374 R35464 H94519 N39798 H8730C R74593 R3173C R34701 HC2982 R32676	GGGGCTGTGA GGGGCTNTTA GGGGCTGTGA GGGGCTGTGA GATTCGGCAC	AACGGAAACACGGAAACACGGAAACACGGAAACA AGGGGAAACA	CAATAATNA GCAATAATTA GCAATAATTA GCAATAATTA GCAATAATTA	CCTGACCAAG CCTGACCAAG CCTGACCAAG CCTGACCAAG CCTGACCAAG CCTGACCAAG	GA GGAGTGC GAAGNAAT GA.GGAGTGC GA.GGAGTGC GA.GGAGTGC GA.GGAGTGC
N57374 R35464 H94519 N39798 H8730C R74593 R3173C R34701 H02982 R32676 T47439	GGGGCTGTGA GGGGCTNTTA GGGGCTGTGA GGGGCTGTGA GATTCGGCAC	AACGGAAACACGGAAACACGGAAACACGGAAACA AGGGGAAACA	CAATAATNA GCAATAATTA GCAATAATTA GCAATAATTA GCAATAATTA	CCTGACCAAG CCTGACCAAG CCTGACCAAG CCTGACCAAG CCTGACCAAG CCTGACCAAG	GA GGAGTGC GAAGNAAT GA.GGAGTGC GA.GGAGTGC GA.GGAGTGC GA.GGAGTGC
N57374 R35464 H94519 N39798 H8730C R74593 R3173C R34701 H02982 R32676 T47439 R73968	GGGGCTGTGA GGGGCTNTTA GGGGCTGTGA GGGGCTGTGA GATTCGGCAC	AACGGAAACACGGAAACACGGAAACA ACGGGAAACA	CAATAATNA GCAATAATTA GCAATAATTA GCAATAATTA GCAATAATTA	CCTGACCAAG CCTGACCAAG CCTGACCAAG CCTGACCAAG CCTGACCAAG CCTGACCAAG	GA GGAGTGC GAAGNAAT GA.GGAGTGC GA.GGAGTGC GA.GGAGTGC GA.GGAGTSC
N57374 R35464 H94519 N39798 H0730C R74593 R3173C R34701 HC2902 R32676 T47439 R73968 H339841	GGGGCTGTGA GGGGCTGTGA GGGGCTGTGA GGGGCTGTGA	AACGGAAACACGGAAACACGGAAACA AGGGGAAACA	CAATAATNA GCAATAATTA GCAATAATTA GCAATAATTA GCAATAATTA	CCTGACCAAG CCTGACCAAG CCTGACCAAG CCTGACCAAG CCTGACCAAG CCTGACCAAG	GA GGAGTGC GAAGNAAT GA.GGAGTGC GA.GGAGTGC GA.GGAGTGC GA.GGAGTGC
N57374 R35464 H94519 N39798 H0730C R74593 R3173C R347C1 HC2902 R32676 T47439 R73966 E339841 H95233	GGGGCTGTGA GGGGCTGTGA GGGGCTGTGA GGGGCTGTGA	AACGGAAACACGGAAACACGGAAACA AGGGGAAACA	CAATAATTA GCAATAATTA GCAATAATTA GCAATAATTA GCAATAATTA	CCTGACCAAG CCTGACCAAG CCTGACCAAG CCTGACCAAG CCTGACCAAG	GA GGAGTGC GAAGNAAT GA.GGAGTGC GA.GGAGTGC GA.GGAGTSC GA.GGAGTSC
N57374 R35464 H94519 N39798 H8730C R74593 R3173C R34701 H02982 R32676 T47439 R73968 H39841 H95233 H39841	GGGGCTGTGA GGGGCTNTTA GGGGCTGTGA GGGGCTGTGA GATTCGGCAC	AACGGAAACACGGAAACACGGAAACA AGGGGAAACA	CAATAATNA GCAATAATTA GCAATAATTA GCAATAATTA GCAATAATTA	CCTGACCAAG CCTGACCAAG CCTGACCAAG CCTGACCAAG CCTGACCAAG CCTGACCAAG	GA GGAGTGC GAAGNAAT GA.GGAGTGC GA.GGAGTGC GA.GGAGTGC GA.GGAGTGC
N57374 R35464 H94519 N39798 H8730C R74593 R3173C R34701 H02982 R32676 T47439 R73966 H39841 H95233 H39841 N3C199	GGGGCTGTGA GGGGCTNTTA GGGGCTGTGA GGGGCTGTGA GATTCGGCAC	AACGGAAACACGGAAACACGGAAACA ACGGGAAACA AGGGGAAACA	CAATAATNA GCAATAATTA GCAATAATTA GCAATAATTA GCAATAATTA	CCTGACCAAG CCTGACCAAG CCTGACCAAG CCTGACCAAG CCTGACCAAG CCTGACCAAG	GA GGAGTGC GAAGNAAT GA.GGAGTGC GA.GGAGTGC GA.GGAGTSC GA.GGAGTSC
N57374 R35464 H94519 N39798 H0730C R74593 R3173C R34701 H02902 R32676 T47439 R73968 £39841 H95233 £39841 N3C199 T52966	GGGGCTGTGA GGGGCTNTTA GGGGCTGTGA GGGGCTGTGA GATTCGGCAC	AACGGAAACACGGAAACACGGAAACA AGGGGAAACA	CAATAATNA GCAATAATTA GCAATAATTA GCAATAATTA GCAATAATTA	CCTGACCAAG CCTGACCAAG CCTGACCAAG CCTGACCAAG CCTGACCAAG CCTGACCAAG	GA GGAGTGC GAAGNAAT GA.GGAGTGC GA.GGAGTGC GA.GGAGTGC GA.GGAGTGC
N57374 R35464 H94519 N39798 H0730C R74593 R3173C R34701 HC2982 R32676 T47439 R73968 H39841 H95233 H39841 N3C199 T52966 N29508	GGGGCTGTGA GGGGCTGTGA GGGGCTGTGA GGGGCTGTGA	AACGGAAACACGGAAACACGGAAACA AGGGGAAACA	CAATAATTA GCAATAATTA GCAATAATTA GCAATAATTA GCAATAATTA	CCTGACCAAG CCTGACCAAG CCTGACCAAG CCTGACCAAG CCTGACCAAG CCTGACCAAG	GA GGAGTGC GAAGNAAT GA.GGAGTGC GA.GGAGTGC GA.GGAGTGC GA.GGAGTGC
N57374 R35464 H94519 N39798 H0730C R74593 R3173C R347C1 HC2982 R32676 T47439 R73968 H39840 H95233 H39841 N3C199 T52966 N29508 N26919	GGGGCTGTGA GGGGCTNTTA GGGGCTGTGA GGGGCTGTGA GATTCGGCAC	AACGGAAACACGGAAACACGGAAACA ACGGGAAACA AGGGGAAACA	CAATAATNA GCAATAATTA GCAATAATTA GCAATAATTA GCAATAATTA	CCTGACCAAG CCTGACCAAG CCTGACCAAG CCTGACCAAG CCTGACCAAG CCTGACCAAG	GA GGAGTGC GAAGNAAT GA.GGAGTGC GA.GGAGTGC GA.GGAGTGC GA.GGAGTGC GA.GGAGTGC
N51374 R35464 H94519 N39798 H8730C R74593 R3113C R34701 H02982 R32676 T47439 R13968 H39841 H95233 H39841 N3C199 T52966 N26919 N26910	GGGGCTGTGA GGGGCTNTTA GGGGCTGTGA GGGGCTGTGA GATTCGGCAC	AACGGAAACACGGAAACACGGAAACA AGGGGAAACA	CAATAATNA GCAATAATTA GCAATAATTA GCAATAATTA GCAATAATTA	CCTGACCAAG CCTGACCAAG CCTGACCAAG CCTGACCAAG CCTGACCAAG CCTGACCAAG	GA GGAGTGC GAAGNAAT GA.GGAGTGC GA.GGAGTGC GA.GGAGTGC GA.GGAGTGC

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R35464 H94519	CAGCAGGAAT CAGCAGGAAT CAGCAGGAAT	GCAGCO GCAGCO GCAGCO	GATT GATT GATT	CCTCTGTCCC CCTCTGTCCC	AAGTGCTCCC AAGTGCTCCC	AGAAGGCAGG AGAAGGCAGG AGAAGGCAGG AGAAGGCAGG
R35464 H94519 N39798 H87300 R74593	CAGCAGGAAT CAGCAGGAAT CAGCAGGAAT CAGCAGGAAT	GCAGCG GCAGCG GCAGCG	GATT GATT GATT	CCTCTGTCCC CCTCTGTCCC CCTCTGTCCC	AAGTGCTCCC AAGTGCTCCC AAGTGCTCCC	AGAAGGCAGG AGAAGGCAGG AGAAGGCAGG AGAAGGCAGG
R35464 H94519 N39798 H87300 R74593 R31130	CAGCAGGAAT CAGCAGGAAT CAGCAGGAAT CAGCAGGAAT CAGCAGGAAT CAGCAGGAAT	GCAGCG GCAGCG GCAGCG	GATT GATT GATT GATT	CCTCTGTCCC CCTCTGTCCC CCTCTGTCCC	AAGTGCTCCC AAGTGCTCCC AAGTGCTCCC AAGT.CTCCC	AGAAGGCAGG AGAAGGCAGG AGAAGGCAGG AGAAGGCAGG
R35464 H94519 N39798 H87300 R74593 R31730 R34701	CAGCAGGAAT CAGCAGGAAT CAGCAGGAAT CAGCAGGAAT CAGCAGGAAT CAGCAGGAAT	GCAGCG GCAGCG GCAGCG GCAGCG	GATT GATT GATT GATT	CCTCTGTCCC CCTCTGTCCC CCTCTGTCCC CCTCTGTCCC CCTCTGTCCC	AAGTGCTCCC AAGTGCTCCC AAGTGCTCCC AAGT.CTCCC	AGAAGGCAGG AGAAGGCAGG AGAAGGCAGG AGAAGGCAGG AGAAGGCAGG
R35464 H94519 N39798 H87300 R74593 R31730 R34701 H32982	CAGCAGGAAT CAGCAGGAAT CAGCAGGAAT CAGCAGGAAT CAGCAGGAAT CAGCAGGAAT	GCAGCG GCAGCG GCAGCG GCAGCG	GATT GATT GATT GATT	CCTCTGTCCC CCTCTGTCCC CCTCTGTCCC CCTCTGTCCC	AAGTGCTCCC AAGTGCTCCC AAGTGCTCCC AAGTGCTCCC	AGAAGGCAGG AGAAGGCAGG AGAAGGCAGG AGAAGGCAGG AGAAGGCAGG
R35464 H94519 N39798 H87300 R74593 R31730 R34701 H32982 R32676	CAGCAGGAAT CAGCAGGAAT CAGCAGGAAT CAGCAGGAAT CAGCAGGAAT CAGCAGGAAT	GCAGCG GCAGCG GCAGCG GCAGCG	GATT GATT GATT GATT	CCTCTGTCCC CCTCTGTCCC CCTCTGTCCC CCTCTGTCCC	AAGTGCTCCC AAGTGCTCCC AAGTGCTCCC AAGT.CTCCC	AGAAGGCAGG AGAAGGCAGG AGAAGGCAGG AGAAGGCAGG AGAAGGCAGG
R35464 H94519 N39798 H87300 R74593 R31730 R34701 H32982 R32676 T47439	CAGCAGGAAT CAGCAGGAAT CAGCAGGAAT CAGCAGGAAT CAGCAGGAAT CAGCAGGAAT	GCAGCG GCAGCG GCAGCG GCAGCG	GATT GATT GATT GATT	CCTCTGTCCC CCTCTGTCCC CCTCTGTCCC CCTCTGTCCC	AAGTGCTCCC AAGTGCTCCC AAGTGCTCCC AAGT.CTCCC	AGAAGGCAGG AGAAGGCAGG AGAAGGCAGG AGAAGGCAGG AGAAGGCAGG
R35464 H94519 N39798 H87300 R74593 R21730 R34701 H32982 R32676 T47439 R73968	CAGCAGGAAT CAGCAGGAAT CAGCAGGAAT CAGCAGGAAT CAGCAGGAAT CAGCAGGAAT	GCAGCG GCAGCG GCAGCG GCAGCG	GATT GATT GATT GATT	CCTCTGTCCC CCTCTGTCCC CCTCTGTCCC CCTCTGTCCC	AAGTGCTCCC AAGTGCTCCC AAGTGCTCCC AAGT.CTCCC	AGAAGGCAGG AGAAGGCAGG AGAAGGCAGG AGAAGGCAGG AGAAGGCAGG
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R35464 H94519 N39798 H87300 R74593 R31730 R34701 H02982 R32676 T47439 R73968 H39840 H95233 A39841	CAGCAGGAAT CAGCAGGAAT CAGCAGGAAT CAGCAGGAAT CAGCAGGAAT	GCAGCG GCAGCG GCAGCG GCAGCG	GATT GATT GATT GATT GATT GATT GATT GATT	CCTCTGTCCC CCTCTGTCCC CCTCTGTCCC CCTCTGTCCC	AAGTGCTCCC AAGTGCTCCC AAGTGCTCCC AAGT.CTCCC	AGAAGGCAGG AGAAGGCAGG AGAAGGCAGG AGAAGGCAGG AGAAGGCAGG
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R35464 H94519 N39798 H87300 R74593 R31730 R34701 H32982 R32676 T47439 R73968 H39840 H95233 R39841 N30199 T52966 N29508	CAGCAGGAAT CAGCAGGAAT CAGCAGGAAT CAGCAGGAAT CAGCAGGAAT CAGCAGGAAT	GCAGCG GCAGCG GCAGCG GCAGCG	GATT GATT GATT GATT GATT GATT GATT GATT	CCTCTGTCCC CCTCTGTCCC CCTCTGTCCC CCTCTGTCCC	AAGTGCTCCC AAGTGCTCCC AAGTGCTCCC AAGT.CTCCC	AGAAGGCAGG AGAAGGCAGG AGAAGGCAGG AGAAGGCAGG AGAAGGCAGG
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H8730C	ATTCT.	SAAG	ACCACTOCA	G CGATATGTT.	CAACTATs	AAGAATACTG
R74593	ATTCT.	SAAG	ACCACTCCA	S CGATATGTT.	CAACTAT G	AAGAATACTS
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Bikunin	CACCGC	c a c	GCAGT CAC	TGGGCC TTG	CCGTG CAT	800 CCTT CCCAC
R35464	CACCGO	CM C	CNATT	: TSGGCC TTG	CCGTG CAT	800 CCTT CCCAC
R35464 H94519	CACCGO GCACCGN GCACCGO	CM C	GNATT GCATT.CAC	: TGGGCCTG	•	CCTT CCCAC
R35464 H94519 N39798	CACCGO GCACCGO . CACCGO	CM C	GNATT GCATT.CAC GCAGT.CAC	: T000000T0	CCGTG CAT	CCTT CCCAC
R35464 H94519 N39798 H873CO	CACCGO GCACCGO .CACCGO	CM C	GNATT GCATT.CAC GCAGT.CAC GCAGTNCAC	7333350TG	C.GTG.CAT.	CCTT.CCCAC CCTTTCCCAC
R35464 H94519 N39798 H87300 R74593	CACCGO GCACCGO .CACCGO	CM C	GNATT GCATT.CAC GCAGT.CAC	7333350TG	C.GTG.CAT.	CCTT.CCCAC CCTTTCCCAC CCTT.CCCAC
R35464 H94519 N39798 H873CO R74593 R3173O	CACCGO GCACCGO .CACCGO	CM C	GNATT GCATT.CAC GCAGT.CAC GCAGTNCAC	7333350TS	C.GTG.CAT. C.GTGGAAT. C.GTGGCATN	CCTT.CCCAC CCTTTCCCAC
R35464 H94519 N39798 H873C0 A74593 R31730 R347C1	CACCGO GCACCGO .CACCGO	CM C	GNATT GCATT.CAC GCAGT.CAC GCAGTNCAC	7333350TS	C.GTG.CAT. C.GTGGAAT. C.GTGGCATN	CCTT.CCCAC CCTTTCCCAC CCTT.CCCAC
R35464 H94519 N39798 H87300 R74593 R31730 R34701 H02982	CACCGO GCACCGO .CACCGO	CM C	GNATT GCATT.CAC GCAGT.CAC GCAGTNCAC	TGGGCCTG	C.GTG.CAT. C.GTGGAAT. C.GTGGCATN	CCTT.CCCAC CCTTTCCCAC CCTT.CCCAC
R35464 H94519 N39798 H873C0 A74593 A31730 A347C1 H02982 R32676	CACCGO GCACCGO .CACCGO	CM C	GNATT GCATT.CAC GCAGT.CAC GCAGTNCAC	TGGGCCTG	C.GTG.CAT. C.GTGGAAT. C.GTGGCATN CCGTG.CAT.	CCTT.CCCAC CCTT.CCCAC CCTT.CCCAC
R35464 H94519 N39798 H873C0 R74593 R3:730 R347C: H02982 R32676 T47439	CACCGO GCACCGO .CACCGO	CAA C	GNATT GCATT.CAC GCAGT.CAC GCAGTNCAC	TGGGCCTG TGGGCC.TTG TGGGCC.TTG	C.GTG.CAT. C.GTGGAAT. C.GTGGCATN CCGTG.CAT.	CCTT.CCCAC CCTTTCCCAC CCTT.CCCAC
R35464 H94519 N39798 H873C0 R74593 R31730 R347C1 H02982 R32676 T47439 R73968	CACCGC GCACCGC CACCGC CACCGC	CAA C	GNATT	TGGGCCTG TGGGCC.TTG TGGGCC.TTG	C.GTG.CAT. C.GTGGAAT. C.GTGGCATN CCGTG.CAT.	CCTT.CCCAC CCTTTCCCAC CCTT.CCCAC
R35464 H94519 N39798 H873C0 A74593 R31730 R347C1 H02982 R32676 T47439 R73968 H39840	CACCGC GCACCGC CACCGC CACCGC	CAA C	GRATT CAS GCAGT.CAS GCAGT.CAS GCAGTNCAS GCAGT.CAS	TGGGCCTG TGGGCC.TTG TGGGCC.TTG	C.GTG.CAT. C.GTGGAAT. C.GTGGCATN CCGTG.CAT.	CCTT.CCCAC CCTTTCCCAC CCTT.CCCAC
R35464 H94519 N39798 H873C0 A74593 A31730 R347C1 H02982 R32676 T47439 R73968 H39840 H95233	CACCGC GCACCGG CACCGC CACCGC	CAA C	GNATT	TGGGCCTG TGGGCC.TTG TGGGCC.TTG	C.GTG.CAT. C.GTGGCAT. C.GTGGCATN CCGTG.CAT.	CCTT.CCCAC CCTTTCCCAC CCTT.CCCAC
R35464 H94519 N39798 H87300 A74593 A31730 R34701 H02982 R32676 T47439 R73968 H39840 H95233 H39841	CACCGC GCACCGC CACCGC CACCGC	CAA C	GNATT	TGGGCCTG TGGGCC.TTG TGGGCC.TTG	C.GTG.CAT. C.GTGGAAT. C.GTGGCATN CCGTG.CAT.	CCTT.CCCAC CCTTTCCCAC CCTT.CCCAC
R35464 H94519 N39798 H873CO R74593 R3173O R347C1 H02982 R32676 T47439 R73968 H39840 H95233 H39841 N30199	CACCGC GCACCGG CACCGC CACCGC	CAA C	GRATT CAS GCAGT CAS GCAGTNCAS GCAGTNCAS	TGGGCCTG TGGGCC.TTG TGGGCC.TTG	C.GTG.CAT. C.GTGGAAT. C.GTGGCATN CCGTG.CAT.	CCTT.CCCAC CCTTTCCCAC CCTT.CCCAC
R35464 H94519 N39798 H87300 A74593 A31730 R34701 H02982 R32676 T47439 R73968 H39840 H95233 H39841	CACCGC GCACCGC CACCGC CACCGC	CAA C	GRATT CAS	TGGGCCTG TGGGCC.TTG TGGGCC.TTG	C.GTG.CAT. C.GTGGAAT. C.GTGGCATN CCGTG.CAT.	CCTT.CCCAC CCTTTCCCAC CCTT.CCCAC
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R35464 H94519 N39798 H87300 R74593 R31730 R34701 H02982 R32676 T47439 R73968 H39840 H39840 H39840 H39841 N30199 T52966 N29508 N26919	CACCGC GCACCGG CACCGC CACCGC	CAA C	GRATT CAS GCAGT CAS GCAGT CAS GCAGT CAS	TGGGCCTG TGGGCC.TTG TGGGCC.TTG	C.GTG.CAT. C.GTGGCATN C.GTGGCATN CCGTG.CAT.	CCTT.CCCAC CCTT.CCCAC CCTT.CCCAC CCTT.CCCAC
R35464 H94519 N39798 H87300 A74593 R31730 R34701 H02982 R32676 T47439 R73968 H39840 495233 H39841 N30199 T52966 N29508	CACCGC GCACCGC .CACCGC .CACCGC	CAA C	GNATT	TGGGCCTG TGGGCC.TTG TGGGCC.TTG	C.GTG.CAT. C.GTGGCATN C.GTGGCATN CCGTG.CAT.	CCTT.CCCAC CCTT.CCCAC CCTT.CCCAC CCTT.CCCAC
R35464 H94519 N39798 H87300 R74593 R31730 R34701 H02982 R32676 T47439 R73968 H39840 H39840 H39840 H39841 N30199 T52966 N29508 N26919	CACCGC GCACCGC .CACCGC .CACCGC	CAA C	GRATT CAS GCAGT CAS GCAGT CAS GCAGT CAS	TGGGCCTG TGGGCC.TTG TGGGCC.TTG TGGGCC.TTG	C.GTG.CAT. C.GTGGCATN C.GTGGCATN CCGTG.CAT.	CCTT.CCCAC CCTT.CCCAC CCTT.CCCAC CCTT.CCCAC
R35464 H94519 N39798 H87300 R74593 R31730 R34701 H02982 R32676 T47439 R73968 H39840 H95233 H39841 N30199 T52966 N29508 N26919 N26910	CACCGC GCACCGC CACCGC CACCGC	CAA C	GNATT GCATT CAS GCAGT CAS GCAGT CAS	TGGGCCTG TGGGCC.TTG TGGGCC.TTG	C.GTG.CAT. C.GTGGAAT. C.GTGGCATN CCGTG.CAT.	CCTT.CCCAC CCTT.CCCAC CCTT.CCCAC CCTT.CCCAC

Fi	gure 40	(Con't	.) -		
• .	801			•	850
aikunin			GA GGAACTC	CTG CAATAA	CTTCATCTAT
H94519	GCTGGTACT				
N39198	GCTGGNAAT				
H87306	GCTNGTACT			CTGGCAATAA	
R74593	GCTGGTACT	T T.GACGTGGA	GA.GGAACTC	CTG.CAATAA	CTTCATCTAT
R31730			• • • • • • • • • • • • • • • • • • • •	• • • • • • • • • • • • • • • • • • • •	
R34701	• • • • • • • • •		• • • • • • • • • • • • • • • • • • • •		
H02982	• • • • • • • • •	GA	GA.GGAACTC	CTG.CAATAA	CTTCATCTAT
R32676 T47439	• • • • • • • • •	• • • • • • • • • • • • • • • • • • • •	• • • • • • • • • •		ATTCGGAA
R73968	• • • • • • • • • •	• • • • • • • • • • • •	• • • • • • • • • •	• • • • • • • • • • • • • • • • • • • •	• • • • • • • • • •
H39840		• • • • • • • • • • •	• • • • • • • • • • • • • • • • • • • •	• • • • • • • • • • • • • • • • • • • •	• • • • • • • • • • • • • • • • • • • •
H95233	• • • • • • • • • •	• • • • • • • • • • •	• • • • • • • • • • • • • • • • • • • •	••••••	• • • • • • • • • • • • • • • • • • • •
H39841	• • • • • • • • • • •	• • • • • • • • • • •	• • • • • • • • • •	• • • • • • • • • • • • • • • • • • • •	
N30199	•••••••	• • • • • • • • • • • • • • • • • • • •	************	• • • • • • • • • • • • • • • • • • • •	• • • • • • • • •
752966	• • • • • • • • • •	• • • • • • • • • • • • • • • • • • • •		• • • • • • • • • • • • • • • • • • • •	
N29508	• • • • • • • • • • • • • • • • • • • •	• • • • • • • • • • • •	• • • • • • • • • •	• • • • • • • • • • • • • • • • • • • •	• • • • • • • • • • • • • • • • • • • •
N26919	• • • • • • • • • • •	• • • • • • • • • • •	• • • • • • • • • •	• • • • • • • • • • • • • • • • • • • •	• • • • • • • • • • • • • • • • • • • •
N26910	• • • • • • • • • • • •	• • • • • • • • • • • • • • • • • • • •	• • • • • • • • • •	• • • • • • • • • • • • • • • • • • • •	• • • • • • • • • • • • • • • • • • • •
H16757	• • • • • • • • • • • • • • • • • • • •	• • • • • • • • • • • • • • • • • • • •	• • • • • • • • • •	••••••	
N27732	• • • • • • • • • • •	• • • • • • • • • • • • • • • • • • • •	• • • • • • • •	• • • • • • • • • • • • • • • • • • • •	• • • • • • • • • • • • • • • • • • • •
114 32					
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	851		••••••		900
Bikunin	851 GGAGGET GE				900 GAGGAGGEST
Bikunin H87300	GGAGGET GE		AAGAACAG C	TACCGCTC T	GAGGAGGCCT
	GGAGGET GE	CGGGGCAAT	AAGAACAG C AAGAACAGNT	TACCGCTC T	GAGGAGGEET TAGGAGGEET
H87300	GGAGGET GE GGAGGETTGE	CGGGGGAAT CGGGGGAATN	AAGAACAG C AAGAACAGNT AAGAACAG.C	TACCGCTC T TACCGCTCTT TACCGCTC.T	GAGGAGGCCT TAGGAGGCCT GAGGAGGCCT
H87300 R74593	GGAGGET GE GGAGGETTGE GGAGGET.GE	CGGGGCAAT CGGGGCAATN CGGGGCCAAT.	AAGAACAG C AAGAACAGNT AAGAACAG.C	TACCGCTC T TACCGCTC.T TACCGCTC.T	GAGGAGGEET TAGGAGGEET GAGGAGGEET GAGGAGGEET
H87300 R74593 R31730	GGAGGET GE GGAGGETTGE GGAGGET.GE	CGGGGCAAT CGGGGCAATN CGGGGCAAT.	AAGAACAG C AAGAACAGNT AAGAACAG.C	TACCGCTC T TACCGCTC.T TACCGCTC.T	GAGGAGGEET TAGGAGGEET GAGGAGGEET GAGGACGEET
H87300 R74593 R31730 R34701	GGAGGET GE GGAGGETTGE GGAGGET GE	CGGGGCAAT CGGGGCAATN CGGGGCAAT	AAGAACAG C AAGAACAGNT AAGAACAG.C	TACCGCTC T TACCGCTC.T TACCGCTC.T TACCGCTC.T	GAGGAGGEET TAGGAGGEET GAGGAGGEET GAGGACGEET
H87300 R74593 R31730 R34701 HC2982	GGAGGCT GC GGAGGCTTGC GGAGGCT.GC	CGSGGCAAT CSGGGCAATN CGGGGCAAT.	AAGAACAG C AAGAACAGNT AAGAACAG C G.C AAGAACA .NC	TACCGCTC T TACCGCTC.T TACCGCTC.T	GAGGAGGEET TAGGAGGEET GAGGAGGEET GAGGAGGEET GAGGAGGEET GAGGAGGEET
H87300 R74593 R31730 R34701 HC2982 R32676	GGAGGCT GC GGAGGCTTGC GGAGGCT.GC	CGGGGCAAT CGGGGCAATN CGGGGCAAT. CGGGG.AAT. CGGGGCAAT.	AAGAACAG C AAGAACAGNT AAGAACAG C G.C AAGAACA .NC	TACCGCTC T TACCGCTC.T TACCGCTC.T TACCGCTC.T TACCGCTC.T	GAGGAGGEET TAGGAGGEET GAGGACGEET GAGGACGEET GAGGACGEET GAGGAGGEET GAGGAGGEET
H87300 R74593 R31730 R34701 HC2982 R32676 T47439	GGAGGCT GC GGAGGCTTGC GGAGGCT.GC	CGGGGCAAT CGGGGCAATN CGGGGCAAT. CGGGG.AAT. CGGGGCCAAT.	AAGAACAG C AAGAACAGNT AAGAACAG C G.C AAGAACA .NC	TACCGCTC T TACCGCTC.T TACCGCTC.T TACCGCTC.T TACCGCTC.T	GAGGAGGEET TAGGAGGEET GAGGAGGEET GAGGAGGEET GAGGAGGEET GAGGAGGEET
H87300 R74593 R31730 R34701 HC2982 R32676 T47439 R73968	GGAGGCT GC GGAGGCTTGC GGAGGCT.GC	CGGGGCAAT CGGGGCAATN CGGGGCAAT. CGGGG.AAT. CGGGGCCAAT.	AAGAACAG C AAGAACAGNT AAGAACAG C G.C AAGAACA .NC	TACCGCTC T TACCGCTC.T TACCGCTC.T TACCGCTC.T TACCGCTC.T	GAGGAGGEET TAGGAGGEET GAGGACGEET GAGGACGEET GAGGACGEET GAGGAGGEET GAGGAGGEET
H87300 R74593 R31730 R34701 HC2982 R32676 T47439 R73968 H39840	GGAGGCT GC GGAGGCTTGC GGAGGCT.GC	CGSGGCAAT CSGGGCAAT. CGGGGCAAT.	AAGAACAG C AAGAACAGNT AAGAACAG.C G.C AAGAACA.NC AAGAACAG.C	TACCGCTC T TACCGCTC.T TACCGCTC.T TACCGCTC.T TACCGCTC.T	GAGGAGGEET TAGGAGGEET GAGGAGGEET GAGGAGGEET GAGGAGGEET GAGGAGGEET
H87300 R74593 R31730 R34701 HC2982 R32676 T47439 R73968 H39840 H95233 H39841 N30199	GGAGGET GE GGAGGET.GE GGAGGET.GE GGAGGET.GE	CGSGGCAAT CSGGGCAAT. CGGGGCAAT.	AAGAACAG C AAGAACAGNT AAGAACAG .C G .C AAGAACA .NC AAGAACAG .C	TACCGCTC T TACCGCTC.T TACCGCTC.T TACCGCTC.T TACCGCTC.T	GAGGAGGEET TAGGAGGEET GAGGACGEET GAGGACGEET GAGGAGGEET GAGGAGGEET GAGGAGGEET
H87300 R74593 R31730 R34701 HC2982 R32676 T47439 R73968 H39840 H95233 H39841	GGAGGCT GC GGAGGCT.GC GGAGGCT.GC GGAGGCT.GC	CGGGGCAAT CGGGGCAAT. CGGGGCAAT. CGGGGCAAT.	AAGAACAG C AAGAACAG.CG.CAAGAACA.NC AAGAACA.C	TACCGCTC T TACCGCTC.T TACCGCTC.T TACCGCTC.T TACCGCTC.T	GAGGAGGEET TAGGAGGEET GAGGAGGEET GAGGAGGEET GAGGAGGEET GAGGAGGEET
H87300 R74593 R31730 R34701 HC2982 R32676 T47439 R73968 H39840 H95233 H39841 N30199	GGAGGCT GC GGAGGCT.GC GGAGGCT.GC GGAGGCT.GC	CGGGGCAAT CGGGGCAAT. CGGGGCAAT. CGGGGCAAT.	AAGAACAG C AAGAACAG.CG.CAAGAACA .NC AAGAACA .NC	TACCGCTC T TACCGCTC.T TACCGCTC.T TACCGCTC.T TACCGCTC.T	GAGGAGGEET TAGGAGGEET GAGGACGEET GAGGACGEET GAGGACGEET GAGGACGEET GAGGACGEET
H87300 R74593 R31730 R34701 HC2982 R32676 T47439 R73968 R39840 H95233 H39841 N30199 T52966	GGAGGCT GC GGAGGCTTGC GGAGGCT.GC GGNGGCT.GC CGAGGAGC	CGGGGCAAT CGGGGCAAT. CGGGGCAAT. CGGGGCAAT.	AAGAACAG C AAGAACAG.CG.CAAGAACA .NC AAGAACA .NC	TACCGCTC T TACCGCTC.T TACCGCTC.T TACCGCTC.T TACCGCTC.T	GAGGAGGEET TAGGAGGEET GAGGAGGEET GAGGAGGEET GAGGAGGEET GAGGAGGEET GAGGAGGEET
H87300 R74593 R31730 R34701 HC2982 R32676 T47439 R73968 H39840 H95233 H39841 N30199 T52966 N29508 N26919	GGAGGCT GC GGAGGCTTGC GGAGGCT.GC GGNGGCT.GC CGAGGAGC	CGGGGCAAT CGGGGCAAT. CGGGGCAAT. CGGGGGAAT.	AAGAACAG C AAGAACAG.CG.CAAGAACA .NC AAGAACAG.C	TACCGCTC T TACCGCTC.T TACCGCTC.T TACCGCTC.T TACCGCTC.T	GAGGAGGEET TAGGAGGEET GAGGAGGEET GAGGAGGEET GAGGAGGEET GAGGAGGEET GAGGAGGEET
H87300 R74593 R31730 R34701 HC2982 R32676 T47439 R73968 H39840 H95233 H39841 N30199 T52966 N29508	GGAGGCT GC GGAGGCTTGC GGAGGCT.GC GGNGGCT.GC	CGSGGCAAT CSGGGCAAT. CGGGGCAAT.	AAGAACAG C AAGAACAG CG.CAAGAACA NC AAGAACA C	TACCGCTC T TACCGCTC.T TACCGCTC.T TACCGCTC.T TACCGCTC.T	GAGGAGGEET TAGGAGGEET GAGGAGGEET GAGGAGGEET GAGGAGGEET GAGGAGGEET GAGGAGGEET

Fi	gure 40	(Con't	.)		
	90:		•		350
Bikunin	SCA TGCT	c cattacttcc	sc		CA GCAGGA
H87300	GCA.T				
R74593	.GCA.TGCT	כ כככדבת::ככ	sc		.CA.GCAGGA
R31730	.SCA.TGCT	- :507607700	sc		.CA.GCAGGA
.R34701			GC.		.CAAGCAGGA
H05985	.GCG .TGCT	COCTGCTTCC	GCTGTGTGTT	CTCTTCCAGG	CCA.GCAGGA
R32676		C CGCTGCTTCC			.CA.GCAGGA
T47439	TGCAGTGCT	COCTGCTTCC	GC		.CA.GCAGGA
R73968	• • • • • • • • • • • • • • • • • • • •				<i>.</i>
HJ9840	••••••	• • • • • • • • • • • • • • • • • • • •			
H95233	•••••			·	
H39841			• • • • • • • • • • • • • • • • • • • •		
N30199	• • • • • • • • • •				
752966	•••••••		• • • • • • • • • • • • • • • • • • • •		
H2 9508	• • • • • • • • • •		• • • • • • • • • • • • • • • • • • • •		
N26919					
N26910			• • • • • • • • • •		• • • • • • • • • • • • • • • • • • • •
H16757	• • • • • • • • • • • •		• • • • • • • • • • • • • • • • • • • •	• • • • • • • • • • • • • • • • • • • •	• • • • • • • • • • • • • • • • • • • •
N27732	••••••	• • • • • • • • • • • • • • • • • • • •	• • • • • • • • • • • • • • • • • • • •	• • • • • • • • • • • • • • • • • • • •	• • • • • • • • • • • • • • • • • • • •
	951				
Bikunin		ccisccccii		222222	:000
R74593	GAA. TCCTCC	CCTGCCCCTT	GGCTCAAAGS	TOCTOCTTC	766 C6666C
R31730		CCTGCCCCTT			TOGECGGGGG
R34701		CCTCCCCCTT		TEGTEGTTCC	TGG.CGGGGC
H02982		CCTCCCCCTT			TGG.CGGGGC
R32676		CCTGCCCCTT			TGG.CGGGGC
747439		CCTGCCCCTT			TGG.CGGGGC
R73968				TEGTEGTTC.	TGG. CGGGGC
ä39840					
H95233				• • • • • • • • • • • • • • • • • • • •	
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H3984;				·········	
H39841 N30139		•••••••		,	
N30139	••••••••••••				
N30199 T52966					
N30139 T52966 N29508					
N30139 T52966 N29508 N26919					

(Con't) :00: 1250 TOTT COTGA TOGTCTTGAT CC T CTTCC TOGG AGCCT CC ATGGTC BIEUNIN R74593 IGITECGIGA IGGIGITGAT CCTT...TCC IGGGGAGCNT CC.ATCGICT R31730 TGTT.CGTGA TGGTGTTGAT CC.T.CTTCC TGGGGAGCCT CC.ATGGTC. R34701 TGTT.CGTGA TGGTGTTGAT CCCTCCTTCC CGGG.AGCCT CCCATGGTCC TGTT.CGTGA TGGTGTTGAT CC.T.CTTCC TGGG.AGCCT CC.ATGGTN. R32676 TGTT.CGTGA TGGTGTTGAT CC.T.CTTCC TGGG.AGCCT CC.ATGGTC. T47439 TGTT.CGTGA TGGTGTTGAT CC.T.CTTCC TGGG.AGCCT CC.ATGGTC. R73968 TGTT.CGTGA TGGTGTTGAT CC.T.CTTCC TGGG.AGCCT CC.ATGGTC. H39840 H95233 H39841 N30199 T52966 N29508 N26919 N26910 H16757 N27732 1051 1100 BIRUNIA TACC TGAT COGGGTGGCA CGGAGG AAC C AGG AGGS TGCCCTGGGC R74593 TAC..TGATT CCGGGTGGCA AGGAGG.AAC C.AGG.AGCG TGCCCTGCGG R31730 TACC.TGAT. CCGGGTGGCA CGGAGGGAAC-C.AGGGAGCG TGCCCTGCGC R34701 TACCCTGAT. CCGGGTGGCA CGGAGG.AAC CCAGG.ANCG TGCCCTGCGC HO2982 TACC. TGAT. CCGGGTNGCA CGGAGG. AAC C. AGGGAGGG TGCCCTGCGN R32676 TACC.TGAT. CCGGGTGGCA CGGAGG.AAC C.AGGGAGCG TGCCCTGCGC T47439 TACC.TGAT. CCGGGTNGCA CGGAGG.AAC C.AGG.AGCG TGCCCTGCGC R73968 TACC.TGAT. CCGGGTGGCA CGGAGG.AAC C.AGG.AGCG TGCCCTGCGC H39640 H95233 **339841** N3C:99 752966 N29508 N26919 N26910 H16757

Figure

Figure 40 (Con't) 1101 1150 BIRUNIN ACCO TOT G GAGOTOCOGA GATGACAAGG AGCAGCTGG TGAAGAAC R74593 ANCS.TCT.G GAGCTTCGGA GATGACAAGG GNT R31730 ACCG.TCTGG GAGCTCCGGA GATGACAAGG GAGCAGCTGG GTGAAGAAC. R3470: ACCG.TCT.G GAGCTCCGGA GATGACAAGG .AGCAGCTGG .TGAAGAAC. HO2982 ACCG. TCTNG GAGCTCCGGA GATGACAAGG .AGCAGCTGG .TGAAGAAC. RJ2676 ACCG.TCTGG GAGCTCCGGA GATGACAAGG GAGCAGCTGG .TGAAGAAC. T47439 ACCG.TCT.G GAGCTCCGGA GATGACAAGG .AGCAGCTGG .TGAAGAAC. R73968 ACCG.TCT.G GAGCTCCGGA GATGACAAGG .AGCAGCTGG .TGAAGAAC. HJ9840 ACCGGTCT.G GAGCTCCGGA GATGACAAGG .AGCAGCTGG .TGAAGAAC. H95233 H39841 NJ0199 ACCG.TCT.G GAGCTCCGGA GATNACAANG .AGCAGCTGN .TGAAGAACC 752966 N29508 N26919 N26910 H16757 N27732 1151 BIRUNIN ACATATOT C CTGT GACCO CCCTGT CGC C AAGAGG A CT GGGGAA 1200 R31730 ACATATGTTC CTGTTGACCG NCCTGTTCGC C.AAGAGG.A TTGGGGGAA. R34701 ACATATGT.C CTGT.GACCG CCCTGT.CGC C.AAGAGG.A CT.GGGGAA. HO2982 ACATATGT.C CTGT.GACCG NCCTGTTCGN C.AAGAGG.A CTNGGGGAAA R32676 ACATATGITC CTGTTGACCG CCCTGTTCGC C.AAGAGGGA NTGGGGGGAA. T47439 ACATATGT.C CTGT.GACCG CCCTGT.CGC C.AAGAGG.A CT.GGGGAA. R73968 ACATATGT.C CTGT.GACCG CCCTGT.CGC C.AAGAGG.A CT.GGGGAA. H39840 ACATATGT.C CTGT.GACCG CCCTGT.CGC C.AAGAGG.A CT.NGCGAA. H95233 N30199 ACATATOTIC CTGT.GACCO-CCCTNT.CGC C.AAGAGG.A CT.GGGNAAA N29508 N26919 N26910 H16757 N27732

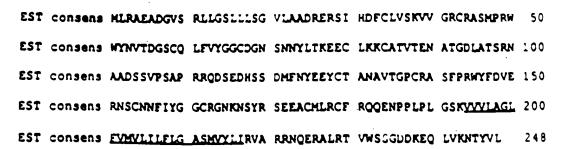
F	igure 40	(Con't)		
	1201				1252
Bikanii	n GGGAGGSS	AGACTAT G	TOT GA SCT	TITITT AA	A TAGA GG
R31730	.GGGAGGGG				
R3470	. GGGAGGGS.	AGACTAT.G.	TGT.GA.GCT	TITITI AA	A.TA
HC2982	CCCCAGGG.	AGATTAT.G.		TTTTTTAA	
R32676	GGGGAGGGG	AGANTATTGT		TITITITAAA	
747439	. GGGAGGGG.	AGACTAT.G.		TTTŢTTAA	
R73968	.GGGAGGGG.	AGACTAT.G.		TTTTTTAA	
H39840	GGGAGGGG.	AGACTAT.G.		AATITTTT	
H95233				• • • • • • • • • •	
H39841	. GGGAGGGGA	AAACHAT.G.		TTTTTT.AAA	
N30199	. GGGAGGNG.	AGACTAT.G.	TGT . AA . GCT	TTTTTTAA	A.TAGAGG
752966	• • • • • • • • • • • • • • • • • • • •				
N2 9508	. GGGAGGGG.	AGACTAG.	TGT . GA . GCT	TTTTTTAA	A.TAGAGG
NS 6919	• • • • • • • • • • • • • • • • • • • •	• • • • • • • • • • • • • • • • • • • •			
N26910		:			
H16757					
N27732	• • • • • • • • • •	••••••	• • • • • • • • • • • • • • • • • • • •		
0	1251				1300
91kunin RJ2676	SATTGACTC		GT GATE A	TTAGGG CT	GAGGTCTSTT
747439	CHITCHITC	GGGNTTTTNA		TTAGGGGGNT	
R73968	GATTGACTC.		GT.GATC.A.	TTAGGGCT	GAGGTCTNTT
H39840		.GGATTTG.A		TTAGGGCT	
H95233	GATTGACTE.	.GGATTTG .A		TTAGGGCT	
H39041	GATTGACTC.			TTAGGGCT	
N30199		.GGATTTG.A		TTAGGGCT	
752966		.GGATTTGGA		TTAGGGCT	GAGGTCTGTT
N29508		CCATTTC			• • • • • • • • • • • • • • • • • • • •
N26919				TTAGGGCT	
N26910			• • • • • • • • • • •	• • • • • • • • • • • • • • • • • • • •	
816757			• • • • • • • • • • •		
N27732				• • • • • • • • • • • • • • • • • • • •	
				• • • • • • • • • • • • • • • • • • • •	
	1301				
Bikunin	TETETEGGAS	GTAGGACGG		S TO TOSCA	:35:
747439	TOTOTHOGAG	STAGGACGA		S IT TOOCA	SSSATSSS
R73968				SCICTICCA	
H3984C	TETETSSGAG	GTAGGACGGC	*******	S. TC. TOSCA	. 555AT5555
H95233	NCTCTGGGAG	NTAGGACGGC	1555777777	G. TC. TGGCA	.555AT555.
H39841	TENETEGGAS	STAGGACGGC	ISSISSION	G. TC. TGGCA	. SSGATSSS.
N30199	TETETEGGAG	STAGGACGGC	1501100	G.TC.TSSCA	COCATOGO.
752966		******		TO TOOCA	COUNTING.
N2 9508	TETETSSSAS	STASSACSSE	TESTICA TO	G.TC.TGGCA	. JOUR LOUD.
N26919					JOURISON
N26910		****			• • • • • • • • • • • • •
H16757				S.TC.TSGCA	********
N27732				GETESTENCA	ACCEATOGG.

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Figure 4C (C n't)
          :351
 Bitunin TITG CITTG G AMICCIC I AGGAGGET CETECT CGC ATGG CC TO
  R73968 TITG.CTTTG GGAAATCCTC TINGGAGGCT CCTCCTTCGC ATGGGCCTTG
  H39840 TTTG.CTTTG GAGAATCCTC T.ANGAGGCT CCTCCT.CGC ATGG.CC.TG
  H95233 TTTG.CTTTG G.AAATCCTC T.AGGAGGCT CCTCCT.CGC ATGG.CC.TG
  H39841 TITG.CITTG G.AAANCCNC T.AGGAGGGT CCTCCT.CGC ATGG.CC.TG
  M30199 TTTG.CTTTG G.AAATCCTC T.AGGAGGCT CCTCCTTCGC ATGG.CC.TG
  152966 TITG.CITTG G.AMATCCTC T.AGGAGGCT CCTCCT.CGC ATGG.CC.TG
  N29508 TITG.CTTTG G.AAATCCTC T.AGGAGGCT CCTCCT.CGC ATGG.CC.TG
  N26919
         ......GAGGCT CCTCCT.CGC ATGG.CC.TG
  N26910 .....CTTTT GNAAATCCTC T.AGGAGGCT CCTCCT.CGC ATGG.CC.TG
 H16757 TTTGCCTTTG G.AAANCCTC T.AGGAGGCT CCTCCT.CGC ATGG.CC.TG
 N27732 TITG.CTTTG G.AAATCCTC TTAGGAGGCT CCTCCT.CGC ATGG.CC.TG
         1401
Bikunin CAGT CT GG CAGCAG CCC CGAGTTGTTT CC TCGCTG ATC GATTTC
 R73968 CAGT.CINGS CAGCANCCCC CGAGTTTTTT TCCTTCGCTG ATCCGATTTC
 H39840 CAGT.CT.GG CAGCAG.CCC CGAGTTGTTT .CC.TCGCTG ATC.GATTTC
 H95233 CAGTTCT..G CAGCAG.CCC CGAGTTGTTT .CC.TCGCTG ATC.GATTTC
 H39841 CAGT.CT.SS CAGCAG.CCC CGAGTTGTTN .CC.TCGCTG ATC.GATNTC
 N30199 CAGT.CT.GG CAGCAG.CCC CGAGTTGTTT .CC.TCGCTG ATC.GATTTC
 T52966 CAGT.CT.GG CAGCAG..CC CGAGTTGTTT .CC.TCGCTG ATC.GATTTC
 N29508 CAGI.CI..G CAGCAG.CCC CGAGTTGTTT .CC.TCGCTG ATC.GATTTC
 N26919 CAGT.CTTCG CAGCAG.CCC CGAGTTGTTT .CC.TCGCTG ANC.GATTTC
N26910 CAGT.CT..G CAGCAG.CCC CGAGTTGTTT .CC.TCGCTG ATCGGATTTC
H16757 CAGINETICS CAGCAGACCE CGAGITGITT .CC.TCGCTG ATC.GATITC
H27732 CAGT.CT.GG CAGCAG.CCC CGAGTTGTTT .CC.TCGCTG ANC.GATTTC
        1451
Bikunin TTT CCTCCA GGTAG AGT TTTC TTTG CTTATGTTGA ATTCCATTGC
R73968 ITTTCCTCCA GGTAAGAATT TTTCTTTT
H39840 TTT.CCTCCA GGTAG..AGT TTTC.TTTG. CTTATGTTGA ATTCCATTGC
H95233 TTT.CCTCCA GGTAG..AGT TTTC.TTTG. CTTATGTTGA ATTCCATTGC
H39841 TTT.CCCCCA GGTAG..AGT TTTC.TTTG. CTTATGTTGA ANTCCATTGC
N30199 TTT.CCTCCA GGTAG..AGT TTTC.TTTG. CTTATGTTGA ATTCCATTGC
T52966 TTT.CCTCCA GGTAG..AGT TTTC.TTTG. CTTATGTTGA ATTCCATTGC
N29508 TIT.CCTCCA GGTAG..AGT TITC.TITG. CTTATGTTGA ATTCCATTGC
N26919 TIT.CONCCA GGTAG..AGT TITC.TITG. CITATGTTGA ATTCCATTGC
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H16757 TITACCCCCA GGTAG. AGT TITECTTTON CITATGTTGA ATTCCATTGC
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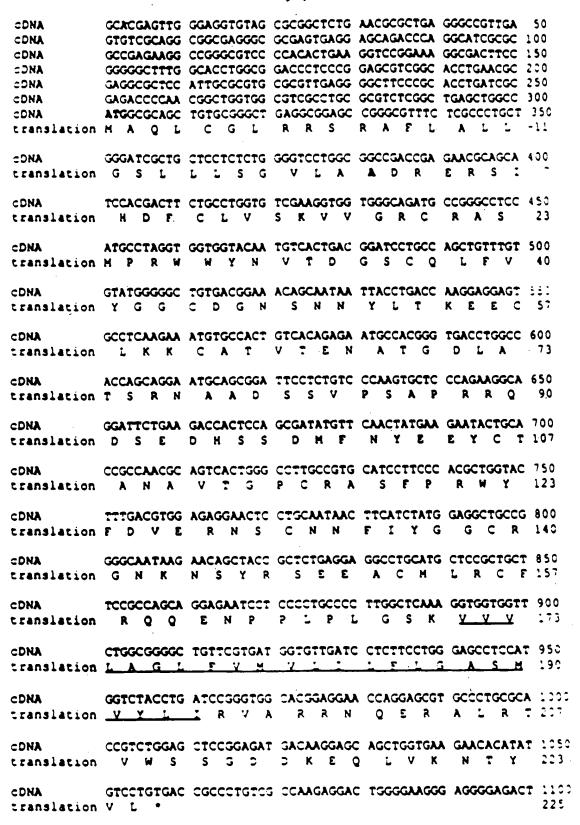
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  N26910 CTCTTTT.CT CATCACAGAA GTGATGTTGG AATCGTTTCT TTTGTTT.GT
  H16757 CICITITACT CATCACAGAA GTGATGTTGG AATCGTTTCT TTTGTTT.GT
  N27732 CTCTTTT.CT CATCACAGAA GTGATGTTGG AATCGTTTCT TTTGTTT.GT
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                                                       1600
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H16757 CTTTAG.AAT AAAAAAAAA AAAAAAAA AAAAAA
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N27732 CTTTAG.AAT AAAAAAAAAA AAAAAAAAA AAAAAAAAA



cDNA translation																ACC T	•	47
cDNA translation	TGA1	rcg(CGAG R D	ACC P	KCD N	C G	CIG	GTC W	GCG1	C R	GCC'	TGC(R	SCG V	TCT(S	EGG(TGA B	٠ -	53 30
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cDNA translation	CCC1	rgc: L	2227 G	ATC S	GCT(SCTC L	CTC	TC1 S	G G	G T V	CCT	GGC A	JGC A	CGA	CCG/ R	AGAJ E	A :	5 3 4
cDNA translation	CGC/ R	NGCI S	ATCC I H	ACG D	ACT' F	TCTG C	CCI	rgg1 V	rgtc S	G A	JAGG V	TGG V	TGG G	GCA R	GAT C	GCC: R	G 2	21
cDNA translation	GGC(STC	CATG M	CCT P	AGGʻ R	TGGT W	GG1	raci	aatg N V	τ	T T	GAC D	gga g	TCC S	TGC C	CAG Q	C Z	253 38
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cDNA translation	GAA(Q	AGGA D	TTC S	TGA E	AGAC D	CA: H	CTC S	CAGC S	:G .	ATA! M	IGT1 F	rcaa N	CT	ATG/ E	NAGI E	W	453 104
cDNA translation	TAC	TGC C	ACCG T A	CCI	LACG	CAGT	CA T	CTG	GGC(e T	TGC(CGT R	GCA1 A S	cc	TTC F	CCA P	CG R	503
cDNA translation	CTG W	GTA Y	CTT1 F	GA(GTG V	GAGA E F	GG R	AAC N	S (7G 5	CAA N	TAA N	CTT(I I	CTA Y	TGG G	AG G	553 138
cDNA translation	GCT	GCC	GGGG	CA N	K K	N N	S AG	CT) Y	ACCG R	CT S	CTG E	AGG E	AGG(C C1	GCA M	TGC L	TC	603
cDNA translation	CGC R	TGC C	TTC	: GC	CAG(AGGI D E	A GA	UT(CCTC P P	cc	CTG L	CCC P	CTT L	G G(TCA S	K	GT Y	653 171
cDNA translation	GGT _Y	GG1	TCT	G GC	GGG(scts	T T:	GT 7	GATG	GT V	GT1	GAT	CCT	C T'	rcc.		3AG A	703 198
cDNA translation	CC1	.cc	igg 1 <u>v</u>	T CT	ACC	TGAT	C C:	SSG V	TGGC	:AC R	GGI	NGG/	NACC	ea G	gag E	CGT R	GCC A	753
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CDNA	TGGCAGGGAT	GGGTTTGCTT	TGGAAATCCT	CTAGGAGGCT	CCTCCTCGCA	1250
CDNA	TGGCCTGCAG	TCTGGCAGCA	GCCCCGAGTT	GTTTCCTCGC	TGATCGATTT	1300
CDNA	CTTTCCTCCA	GGTAGAGTTT	TCTTTGCTTA	TGTTGAATTC	CATTGCCTCC	1350
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CDNA	GAAGGAAAGT	AAAATGTACA	AGTTTAATAA	AAAGGGGCCT	TCCCCTTTAG	1500
CDNA	AATAAATTTC	CAGCATGTTG	CTTTCAAAAA	********	***	
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F.C						
EST consens			MLR	AEADGVSRLL	GSLLLSGVLA	-:
PCR clone			MAQLCGL	RRSRAFLALL	GSLLLSGVLA	- 1
ycony clou					GSLLLSGVLA	
EST consens	ADRERSINDE	CLVSKVVGRC	RASMPRWWYN	VTDGSCOLFV	YGGCDGNSNN	50
PCR clone	ADRERSINDE	CLVSKVVGRC	RASMPRIMIYN	VTDGSCOLEV	VCCCDCHSNN	50
Acona clone	ADRERSTHOF	CLVSKVVGRC	BYCHBBAMAN	VTDGSCQLEV	VCCCDCHSHN	50
		oz o	INDIE KANTI	110030022	100CDGH3HH	20
EST consens	YLTREECLKK	CATVTENATG	DLATSRNAAD	SSVPSAF RRO	DSEDHSSDMF	100
PCR clone	YLTKEECLKK	CATVTENATG	DLATSRNAAD	SSVPSAPRRO	DSEDHSSDMF	100
ACDNA clone	YLTKEECLKK	CATVTENATG	DLATSRNAAD	SSVPSAPRRQ	DSEDHSSDMF	100
EST consens	NYFFYCTANA	VTCDCDACED	BUVERUPANC	CARTINGGO	COROLEVACE	
PCR clone	NYPEYCTANA	ALCICIONSEL	WATEDATEM?	CHAPTIGGCK	GNANSTRSEE	150
JOHNA GLOSS	MIEEICIANA	VIGPCIASEP	WALLDAFKW2	CNNFITGGCR	GNENSTRSEE	:50
AcDNA clone	NIEEICTANA	VTGPCRASFP	RWYFDVERNS	CNNFIYGGCR	GNKNSYRSEE	150
EST consens	ACHLRCFRQQ	ENPPLPLGSK	VVVLAGLEVM	VLILFLGASH	YYLIRVARRN	200
PCR clone	ACMLRCFROO	ENPPLPLGSK	VVVLAGLEVM	"LILFLGASM	VYLIRVARRN	200
AcDNA clone	ACMLRCFROO	ENPPLPLGSK	VVVIAGIEVM	UTTIFICACH	UVI IBUADON	200
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EST consens	QERALRTVWS	SGDDKEOLVK	NTYVL			225
PCR clone	QERALRTVWS					213
CDNA clone			NTYUI			
	#	SASSUESSELV	17 A A A D			225

Purification of Placental Bikunin using Superdex 75 Gel-Filtration

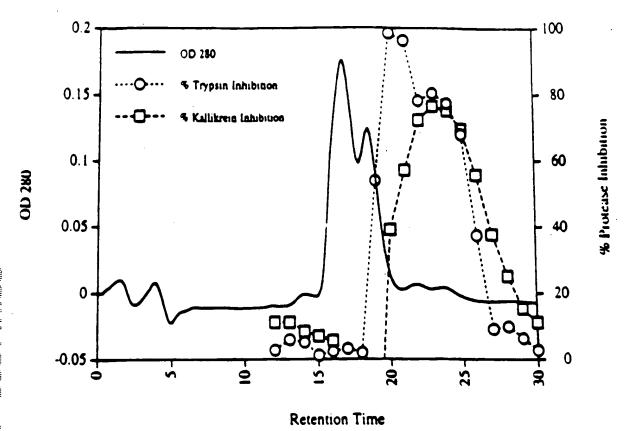


FIGURE 5



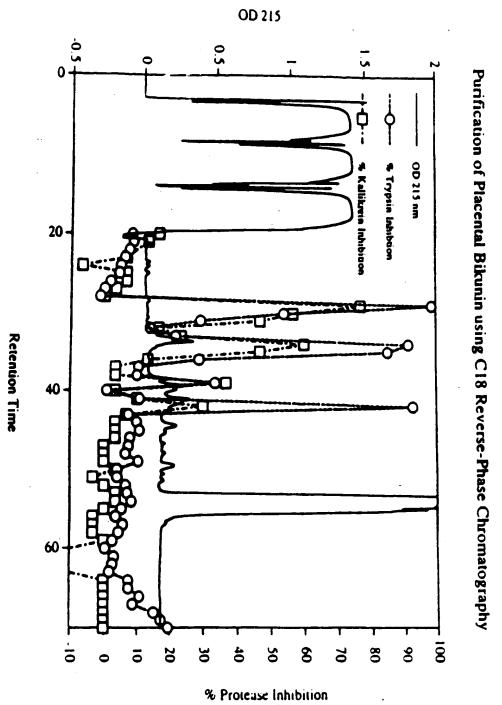


Figure 7

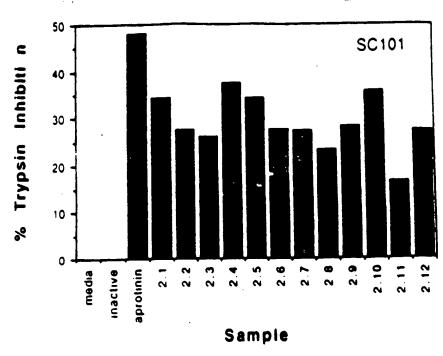


Figure 8B

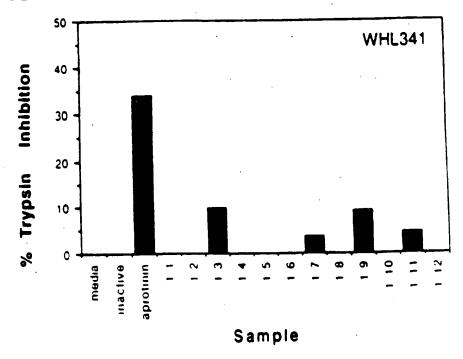
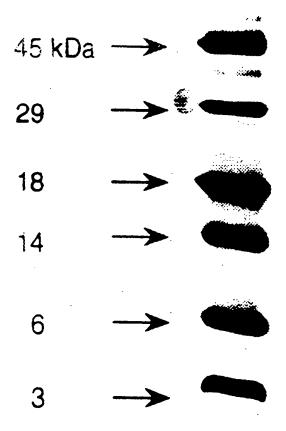
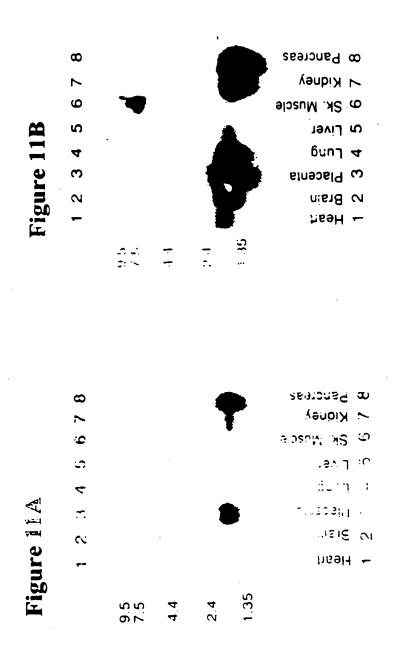


Figure 10





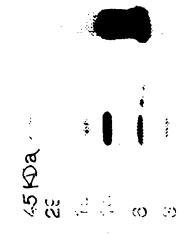


2 3 4

Figure 12B

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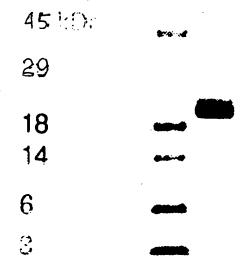
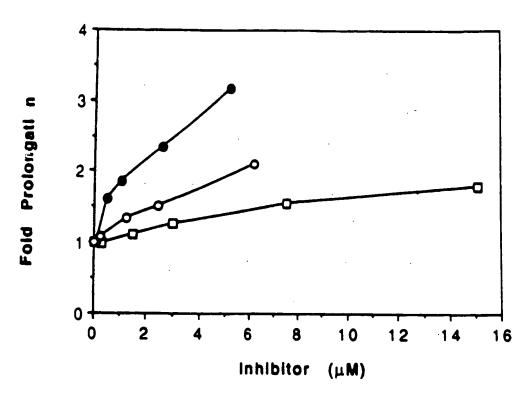
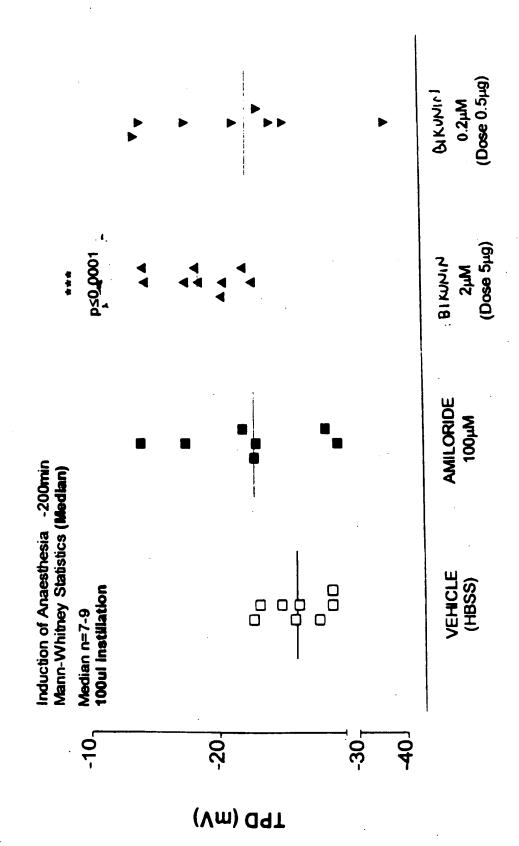


Figure 14

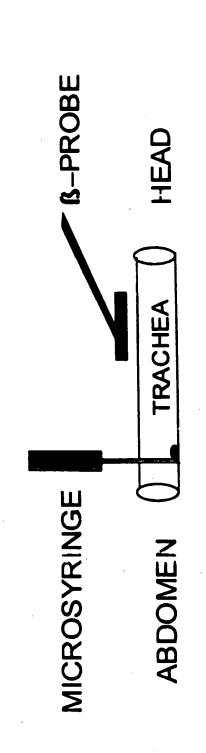


(0.2-2uM) and amiloride (100uM) on tracheal potential difference (TPD) 3 hours post treatment Figure 15: The effect of BIKUNIN



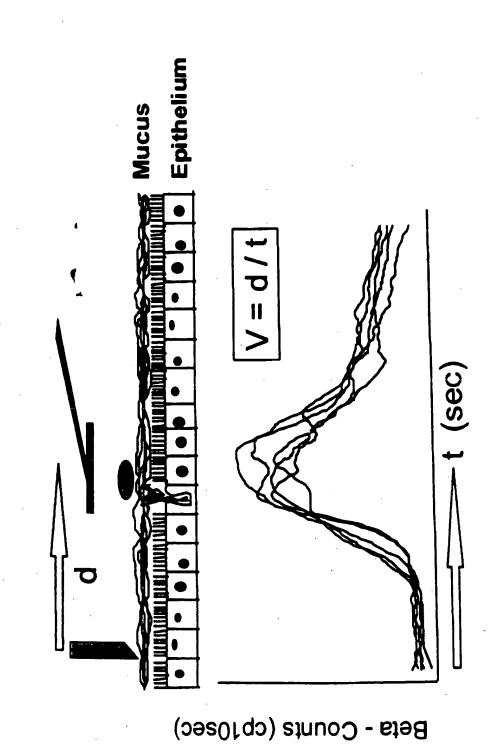
TREATMENT

Figure 16 (a): Diagram to show the arrangement of needle and Beta probe.

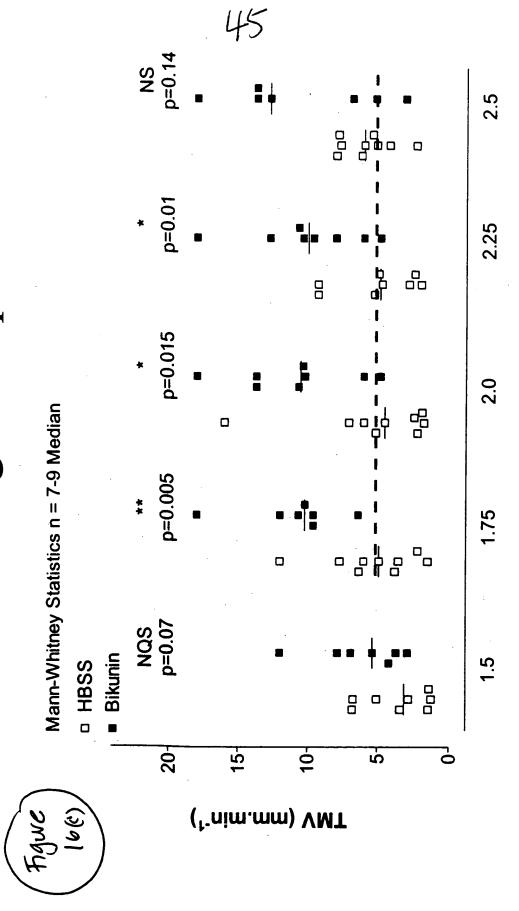


Longitudinal view

Figure 16 (b): Counts detected by the probe as the ³²P-labeled Saccharomyces cerevisiae are transported along the tracheal mucociliary layer.



Sustained Increase in Tracheal Mucus Velocity In Vivo in Guinea Pig in Response to Bikunin



(1

TIME (HOURS) FROM TOPICAL TREATMENT

(70nM) on sodium dependent current in cultured normal Figure 17: Short circuit current (Isc) trace to show the action of human bronchial epithelial cells in vitro BIKUNIN

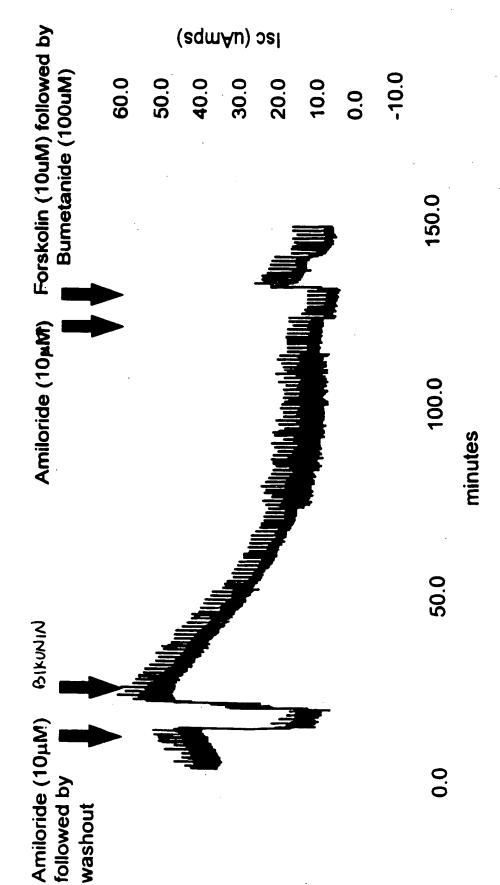
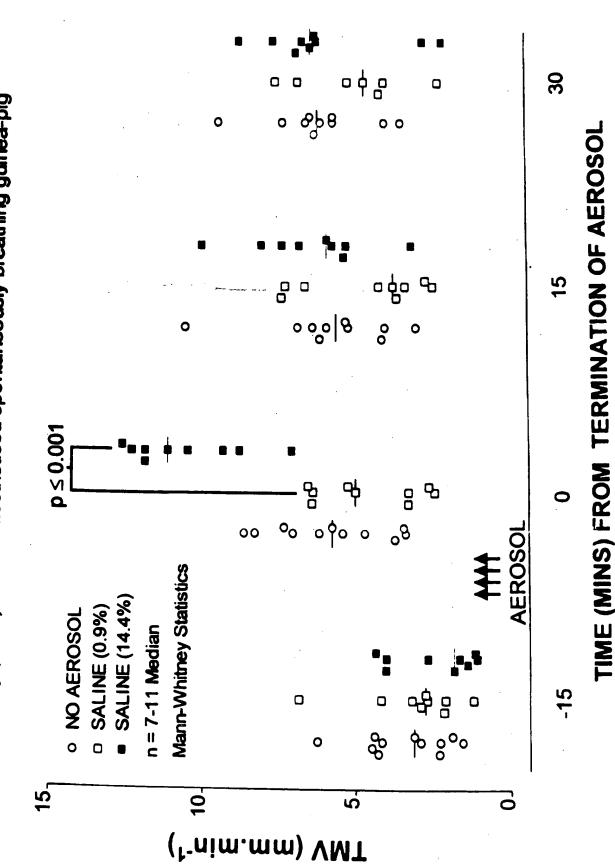
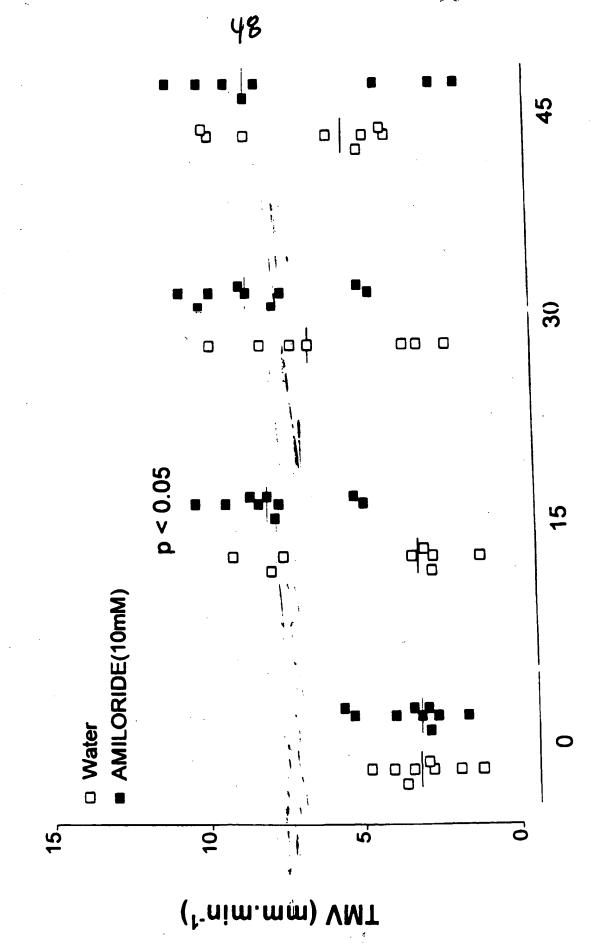
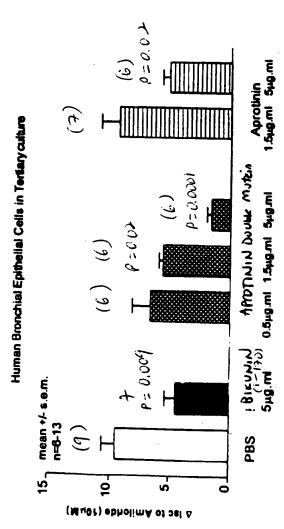


Figure 18 : The effect of a 5 min aerosol of hypertonic saline (14.4%) on tracheal mucus velocity (TMV) in the anaesthetised spontaneously breathing guinea-pig



mucus velocity (TMV) in the anaesthetised spontaneously breathing guinea-pig Figure 19: The effect of a 20 min aerosol of amiloride (10mM) on tracheal





(5ug/mL) and Aprotinin (5 ug/mL) inhibit sodium dependent short circu current (Isc) in normal human bronchial epithelial cells in vitro at 90 Figure 20: Aprotinin double mutein (0.5 - 5 ug/mL), Bikurin (1-170) minutes following treatment.

(1 mg/mL) on sodium dependent current in cultured cystic fibrosis human Figure 21 Short circuit current (Isc) trace to show the action of aprotinin bronchial epithelial cells in vitro

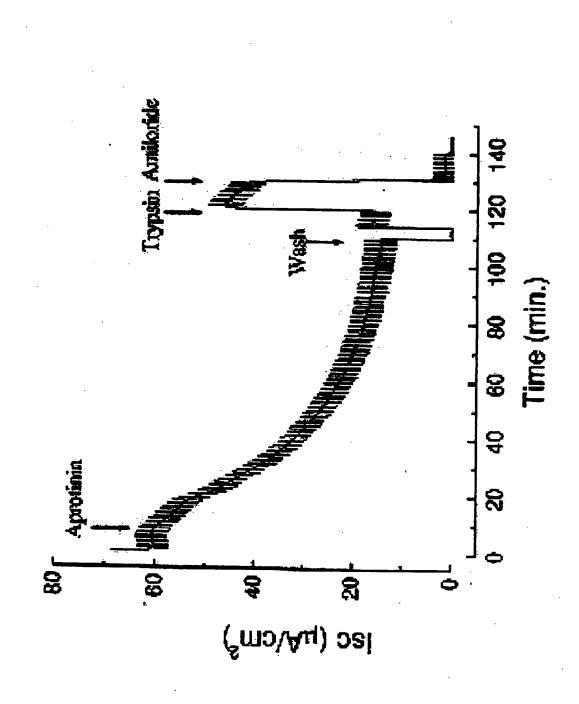


Figure 22: 9mg CHO mBikunin (1-170) aerosol (3 ml. of 3 mg/mL) increased tracheal mucus velocity in sheep (n=6) at 0, 0.5, 3, compared to animals (n=6) receiving PBS vehicle

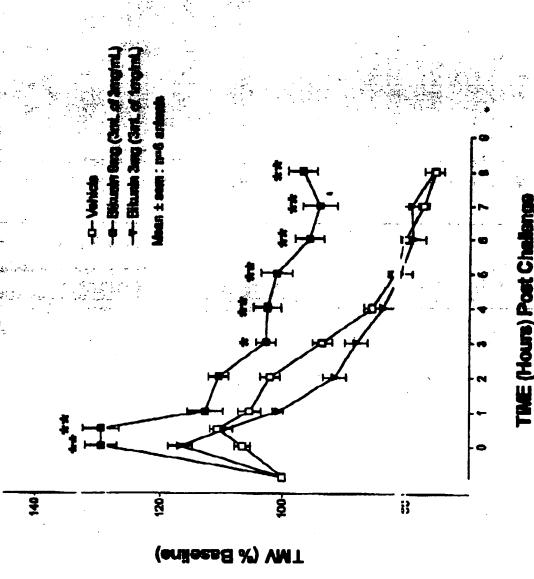


Figure 23: The effect of a 30 minute pre-treatment of Bikunin (50 amiloride (30uM) in cultured guinea-pig tracheal epithelial cells and 10 ug/mL) on the short circuit current (Δ Isc) response to

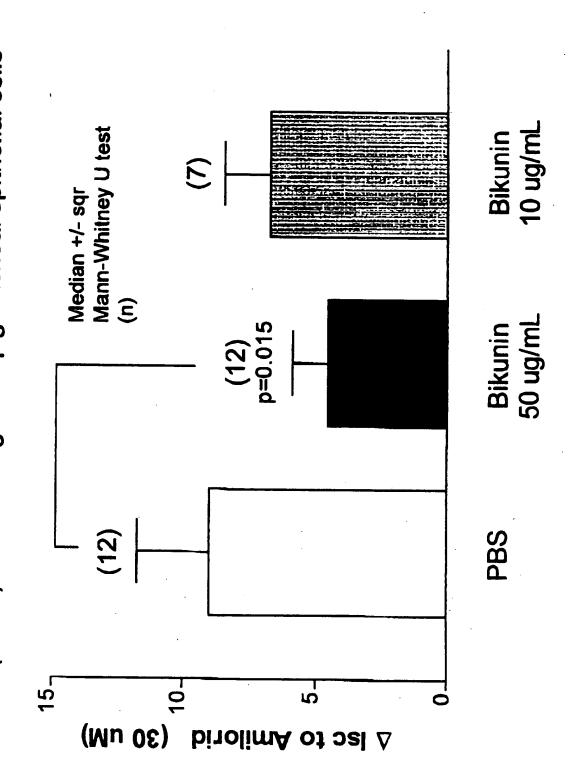


Figure 34: The effect of a 90 minute pre-treatment of Bikunin (100 and 50 ug/mL) on the short circuit current (Δ Isc) response to amiloride (10 uM) in cultured Ovine tracheal epithelial cells

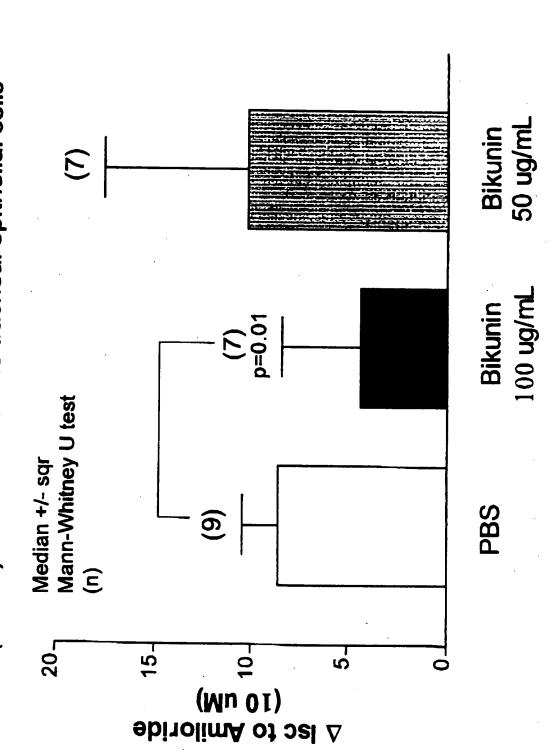


Figure 354): The Effect of LPS (0.03 mg/mL x 10 min) on neutrophil numbers in bronchoalveolar lavage fluid (BALF) of the guinea-pig 24 hours post challenge

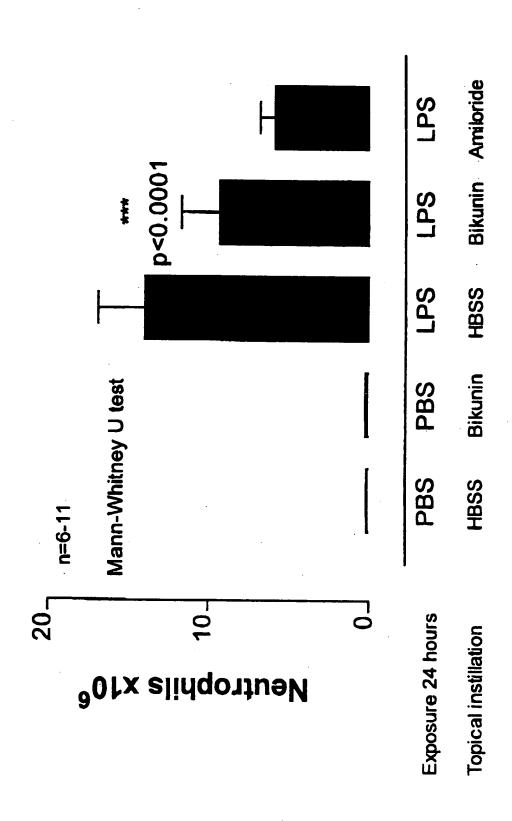


Figure 25'4 : The Effect of Bikunin (50 ug/mL) on Tracheal Potential Difference (TPD) in Guinea-Pigs pre-exposed to LPS (0.03 mg/mL x 10 min)

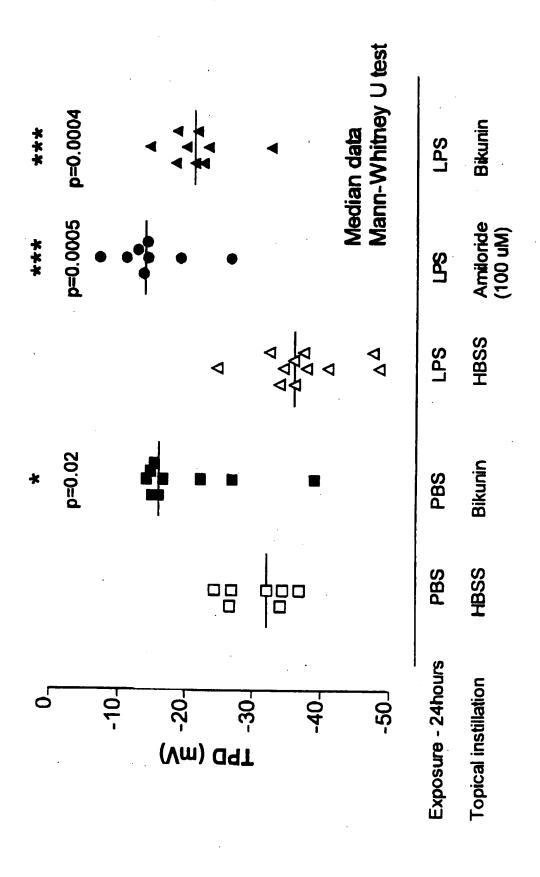
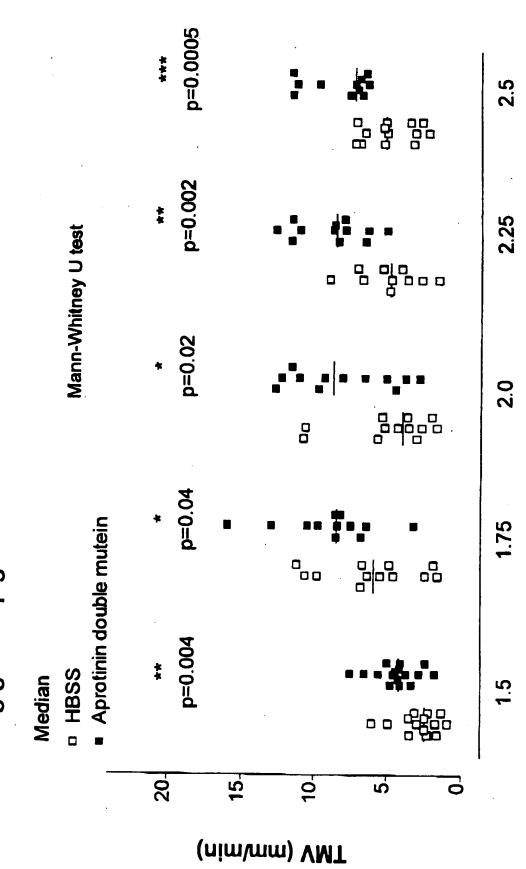


Figure 26: The effect of Aprotinin double mutein (10 ug) on tracheal mucus velocity (TMV) in the anaesthetised spontaneously breathing guinea-pig



TIME (HOURS) FROM TOPICAL TREATMENT

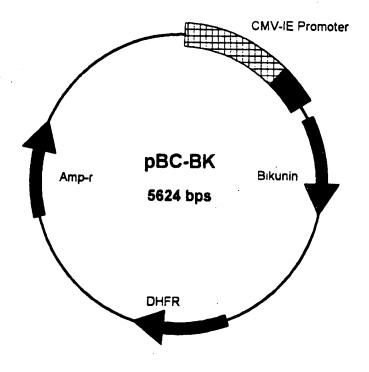


Figure 27

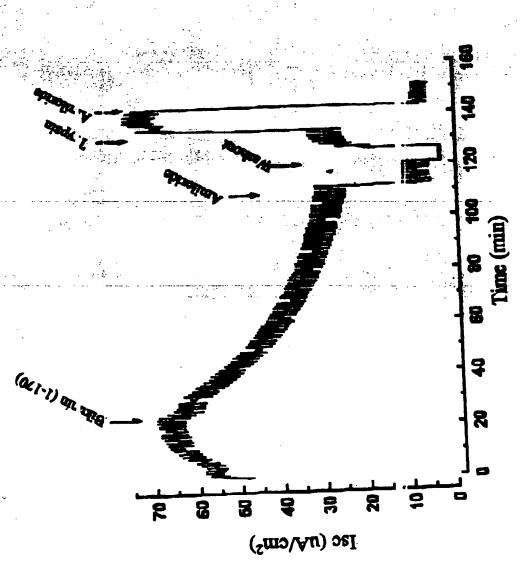
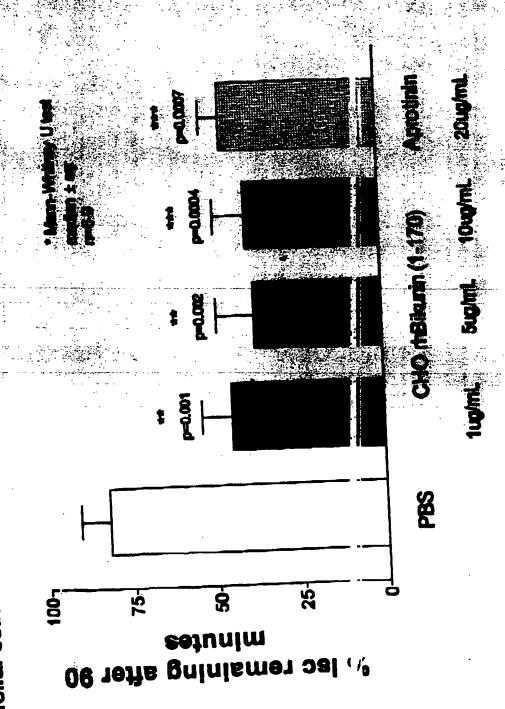


Figure 28(b): Percentage baseline short circuit current (lec) remaining at 90 minutes after pretreatment with PBS, CHO mBilkunn (F170) (10 ug/mL - 10 ug/mL) or Aprotinin (20 ug/mL) in cystic fibraris bronchial epithelial cells in vitro



Flow Chart of CHO rhBikunin Purification Process Train

CHO TCF

SP-Sepharose, pH 5, Capture

UF/DF/Fil., pH 8.2, Concentration & Buffer Exchange

Q-Sepharose, pH 8.2, Capture, Dimer removal

Zn-IMAC, pH 7.2, Flowthrough, CHO protein removal

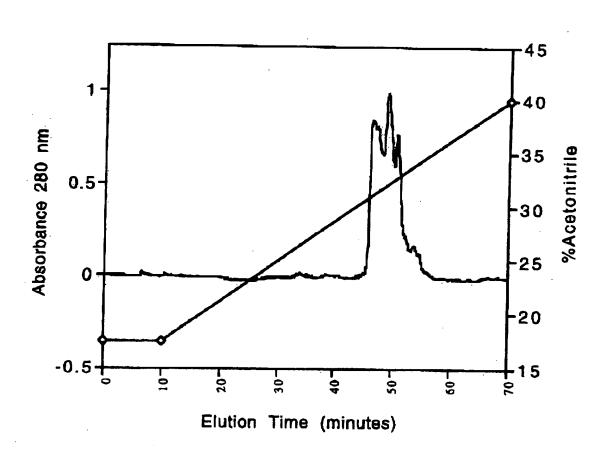
UF, pH 7.4, Concentration

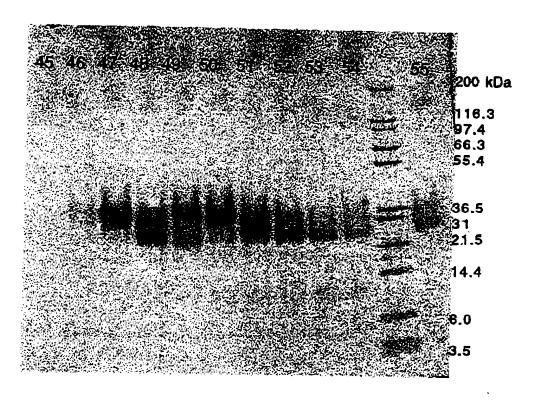
S-200, pH 7.2, Size Exclusion

ETOX Treatment, pH 7.2, Protective Pyrogen Removal

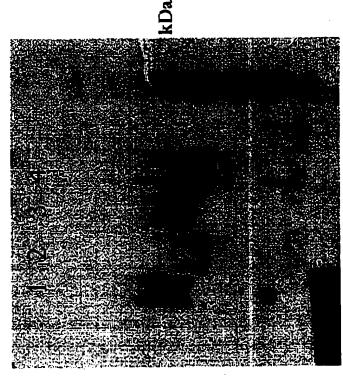
Figure 29

Figure & 30(a)





Deglycosylation of CHO-derived Bikunin



2: "High" MW bikunin post N-Olycosidase F Lane 1: "High" MW bikunin prior to treatment

3: "Low" MW bikunin prior to treatment 4: "Low" MW bikunin post N-Glycosidase F